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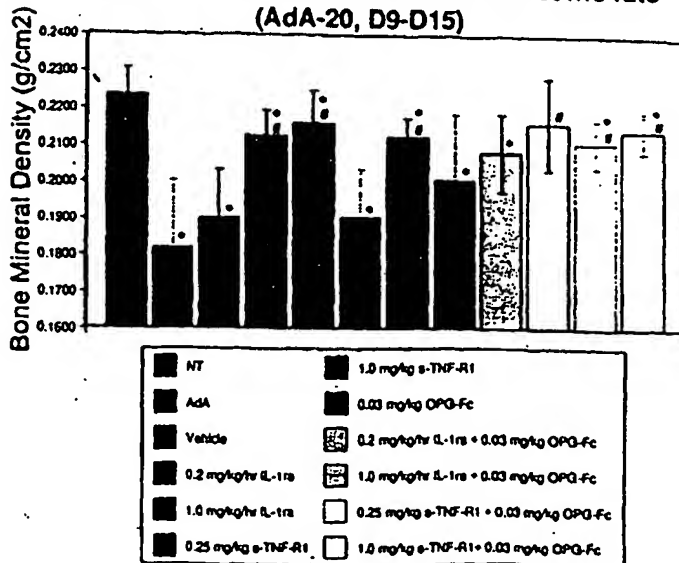
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(54) Title: COMBINATION THERAPY FOR CONDITIONS LEADING TO BONE LOSS

Combination treatment with OPG-Fc and IL-1ra or s-TNF-R1 on adjuvant arthritis in male Lewis rats (AdA-20, D9-D15)



Pairs from rats with adjuvant arthritis induced by 0.5mg mycobacteria in oil were analyzed by DEXA for BMD. Evaluation of BMD, a 20mm X 25mm was centered at the tibiotarsal region. (sept AdA-20 5/93, Amgen nbr/22937 p68).  
\* compared to normal, # compared to vehicle  
P < 0.05 Mann-Whitney U test.

(57) Abstract: The present invention discloses a novel secreted polypeptide, termed osteoprotegerin, which is a member of the tumor necrosis factor receptor superfamily and is involved in the regulation of bone metabolism. Also disclosed are nucleic acids encoding osteoprotegerin, polypeptides, recombinant vectors and host cells for expression, antibodies which bind OPG, and pharmaceutical compositions. The polypeptides are used to treat bone diseases characterized by increased resorption such as osteoporosis. Methods of treatment are described using the polypeptides in conjunction with various agents, including IL-1 inhibitors, TNF- $\alpha$  inhibitors, and serine protease inhibitors.

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## COMBINATION THERAPY FOR CONDITIONS LEADING TO BONE LOSS

### Cross-Reference to Related Applications

5        This application is a continuation-in-part of U.S.  
Ser. No. 09/350,670 filed July 9, 1999, which is a  
continuation-in-part (CIP) of U.S. Ser. No. 08/706,945,  
filed on September 3, 1996; which in turn is a CIP of  
U.S. Ser. No. 08/577,788, filed December 22, 1995. Each  
10 of the foregoing applications is hereby incorporated by  
reference.

### Field of the Invention

The invention relates generally to polypeptides  
involved in the regulation of bone metabolism. More  
15 particularly, the invention relates to a novel  
polypeptide, termed osteoprotegerin, which is a member  
of the tumor necrosis factor receptor superfamily. The  
polypeptide is used to treat bone diseases  
characterized by increased bone loss such as  
20 osteoporosis and arthritis.

### Background of the Invention

Polypeptide growth factors and cytokines are  
secreted factors which signal a wide variety of changes  
in cell growth, differentiation, and metabolism, by  
25 specifically binding to discrete, surface bound  
receptors. As a class of proteins, receptors vary in  
their structure and mode of signal transduction. They  
are characterized by having an extracellular domain  
that is involved in ligand binding, and cytoplasmic  
30 domain which transmits an appropriate intracellular  
signal. Receptor expression patterns ultimately  
determine which cells will respond to a given ligand,  
while the structure of a given receptor dictates the  
cellular response induced by ligand binding. Receptors  
35 have been shown to transmit intracellular signals via



their cytoplasmic domains by activating protein tyrosine, or protein serine/threonine phosphorylation (e.g., platelet derived growth factor receptor (PDGFR) or transforming growth factor- $\beta$  receptor-I (TGF $\beta$ R-I),

5 by stimulating G-protein activation (e.g.,  $\beta$ -adrenergic receptor), and by modulating associations with cytoplasmic signal transducing proteins (e.g., TNFR-I and Fas/APO) (Heldin, *Cell* 80, 213-223 (1995)).

The tumor necrosis factor receptor (TNFR)

10 superfamily is a group of type I transmembrane proteins which share a conserved cysteine-rich motif which is repeated three to six times in the extracellular domain (Smith, *et al.* *Cell* 76, 953-962 (1994)). Collectively, these repeat units form the ligand binding domains of

15 these receptors (Chen *et al.*, *Chemistry* 270, 2874-2878 (1995)). The ligands for these receptors are a structurally related group of proteins homologous to TNF $\alpha$ . (Goeddel *et al.* *Cold Spring Harbor Symp. Quart. Biol.* 51, 597-609 (1986); Nagata *et al.* *Science* 267,

20 1449-1456 (1995)). TNF $\alpha$  binds to distinct, but closely related receptors, TNFR-I and TNFR-II. TNF $\alpha$  produces a variety of biological responses in receptor bearing cells, including, proliferation, differentiation, and cytotoxicity and apoptosis (Beutler *et al.* *Ann. Rev.*

25 *Biochem.* 57, 505-518 (1988)).

TNF $\alpha$  is believed to mediate acute and chronic inflammatory responses (Beutler *et al.* *Ann. Rev. Biochem.* 57, 505-508 (1988)). Systemic delivery of TNF $\alpha$  induces toxic shock and widespread tissue necrosis.

30 Because of this, TNF $\alpha$  may be responsible for the severe morbidity and mortality associated with a variety of infectious diseases, including sepsis. Mutations in FasL, the ligand for the TNFR-related receptor Fas/APO (Suda *et al.* *Cell* 75, 1169-1178 (1993)), is associated



with autoimmunity (Fisher *et al.* Cell 81, 935-946 (1995)), while overproduction of FasL may be implicated in drug-induced hepatitis. Thus, ligands to the various TNFR-related proteins often mediate the serious effects  
5 of many disease states, which suggests that agents that neutralize the activity of these ligands would have therapeutic value. Soluble TNFR-I receptors, and antibodies that bind TNF $\alpha$ , have been tested for their ability to neutralize systemic TNF $\alpha$  (Loetscher *et al.*  
10 Cancer Cells 3(6), 221-226 (1991)). A naturally occurring form of a secreted TNFR-I mRNA was cloned, and its product tested for its ability to neutralize TNF $\alpha$  activity *in vitro* and *in vivo* (Kohno *et al.* PNAS USA 87, 8331-8335 (1990)). The ability of this protein  
15 to neutralize TNF $\alpha$  suggests that soluble TNF receptors function to bind and clear TNF thereby blocking the cytotoxic effects on TNFR- bearing cells.

An object of the invention is to identify new members of the TNFR superfamily. It is anticipated that  
20 new family members may be transmembrane proteins or soluble forms thereof comprising extracellular domains and lacking transmembrane and cytoplasmic domains. We have identified a new member of the TNFR superfamily which encodes a secreted protein that is closely  
25 related to TNFR-II. By analogy to soluble TNFR-II, the TNFR-II related protein may negatively regulate the activity of its ligand, and thus may be useful in the treatment of certain human diseases.

A further object of this invention is new methods  
30 of treatment of inflammatory diseases and medical conditions.

#### Summary of the Invention

A novel member of the tumor necrosis factor receptor (TNFR) superfamily has been identified from a  
35 fetal rat intestinal cDNA library. A full-length cDNA



clone was obtained and sequenced. Expression of the rat  
cDNA in a transgenic mouse revealed a marked increase  
in bone density, particularly in long bones, pelvic  
bone and vertebrae. The polypeptide encoded by the cDNA  
5 is termed Osteoprotegerin (OPG) and plays a role in  
promoting bone accumulation.

The invention provides for nucleic acids encoding  
a polypeptide having at least one of the biological  
activities of OPG. Nucleic acids which hybridize to  
10 nucleic acids encoding mouse, rat or human OPG as shown  
in Figures 2B-2C (SEQ ID NO:120), 9A-9B (SEQ ID NO:  
122), and 9C-9D (SEQ ID NO: 124) are also provided.  
Preferably, OPG is mammalian OPG and more preferably is  
human OPG. Recombinant vectors and host cells  
15 expressing OPG are also encompassed as are methods of  
producing recombinant OPG. Antibodies or fragments  
thereof which specifically bind the polypeptide are  
also disclosed.

Methods of treating bone diseases are also  
20 provided by the invention. The polypeptides are useful  
for preventing bone resorption and may be used to treat  
any condition resulting in bone loss such as  
osteoporosis, hypercalcemia, Paget's disease of bone,  
and bone loss due to rheumatoid arthritis or  
25 osteomyelitis, and the like. Bone diseases may also be  
treated with anti-sense or gene therapy using nucleic  
acids of the invention. Pharmaceutical compositions  
comprising OPG nucleic acids and polypeptides are also  
encompassed.

30 The invention relates further to treatment of  
diseases using combination therapy. In particular, the  
novel polypeptides described herein may be used in  
conjunction with bone morphogenic proteins BMP-1  
through BMP-12; TGF- $\beta$  and TGF- $\beta$  family members; IL-1  
35 inhibitors; TNF- $\alpha$  inhibitors; parathyroid hormone and



analogs thereof; parathyroid related protein and  
analogs thereof; E series prostaglandins;  
bisphosphonates; bone-enhancing minerals; NSAIDs;  
immunosuppressants; serine protease inhibitors; IL-6  
5 inhibitors; IL-8 inhibitors (e.g., antibodies to IL-8);  
IL-18 inhibitors; ICE modulators; FGF-1 to FGF-10; FGF  
modulators; PAF antagonists; KGF, KGF-related  
molecules, or KGF modulators; MMP modulators; NOS  
modulators; modulators of glucocorticoid receptor;  
10 modulators of glutamate receptor; modulators of LPS  
levels; and noradrenaline and modulators and mimetics  
thereof.

#### Description of the Figures

Figure 1. A. FASTA analysis of novel EST LORF.  
15 Shown is the deduced FRI-1 amino acid sequence aligned  
to the human TNFR-II sequence. B. Profile analysis of  
the novel EST LORF shown is the deduced FRI-1 amino  
acid sequence aligned to the TNFR-profile. C.  
Structural view of TNFR superfamily indicating region  
20 which is homologous to the novel FRI-1.

Figure 2. Structure and sequence of full length  
rat OPG gene, a novel member of the TNFR superfamily.  
A. Map of pMOB-B1.1 insert. Box indicates position of  
LORF within the cDNA sequence (bold line). Black box  
25 indicates signal peptide, and gray ellipses indicate  
position of cysteine-rich repeat sequences. B, C.  
Nucleic acid and protein sequence of the Rat OPG cDNA.  
The predicted signal peptide is underlined, and  
potential sites of N-linked glycosylation are indicated  
30 in bold, underlined letters. D, E. Pileup sequence  
comparison (Wisconsin GCG Package, Version 8.1) of OPG  
with other members of the TNFR superfamily, fas (SEQ ID  
NO:128); tnfr1 (SEQ ID NO: 129); sfu-t2 (SEQ ID  
NO:130); tnfr2 (SEQ ID NO:131); cd40 (SEQ ID NO:132);  
35 osteo (SEQ ID NO:133); ngfr (SEQ ID NO:134); ox40 (SEQ  
ID NO:135); 41bb (SEQ ID NO:136).



Figure 3. PepPlot analysis (Wisconsin GCG Package, Version 8.1) of the predicted rat OPG sequence. A. Schematic representation of rat OPG showing hydrophobic (up) and hydrophilic (down) amino acids. Also shown are basic (up) and acidic (down) amino acids. B. Display of amino acid residues that are beta-sheet forming (up) and beta-sheet breaking down) as defined by Chou and Fasman (Adv. Enz. 47, 45-147 (1948)). C. Display of propensity measures for alpha-helix and beta-sheet (Chou and Fasman, ibid). Curves above 1.00 show propensity for alpha-helix or beta-sheet structure. Structure may terminate in regions of protein where curves drop below 1.00. D. Display of residues that are alpha-forming (up) or alpha-breaking (down). E. Display of portions of the protein sequence that resemble sequences typically found at the amino end of alpha and beta structures (Chou and Fasman, ibid). F. Display of portions of the protein sequence that resemble sequences typically found at the carboxyl end of alpha and beta structures (Chou and Fasman, ibid). G. Display of portions of the proteins sequence typically found in turns (Chou and Fasman, ibid) H. Display of the helical hydrophobic moment (Eisenberg et al. Proc. Natl. Acad. Sci. USA 81, 140-144 (1984)) at each position in the sequence. I. Display of average hydrophathy based upon Kyte and Doolittle (J. Mol. Biol. 157, 105-132 (1982)) and Goldman et al. (reviewed in Ann. Rev. Biophys. Biophys. Chem. 15, 321-353 (1986)).

Figure 4. mRNA expression patterns for the OPG cDNA in human tissues. Northern blots were probed with a 32P-labeled rat cDNA insert (A, left two panels), or with the human cDNA insert (B, right panel).

Figure 5. Creation of transgenic mice expressing the OPG cDNA in hepatocytes. Northern blot expression of HE-OPG transgene in mouse liver.



Figure 6. Increase in bone density in OPG transgenic mice. Panel A-F. Control Mice. G-J, OPG expressing mice. At necropsy, all animals were radiographed and photographs prepared. In A-F, the radiographs of the control animals and the one transgenic non-expressor (#28) are shown. Note that the bones have a clearly defined cortex and a lucent central marrow cavity. In contrast, the OPG (G-J) animals have a poorly defined cortex and increased density in the marrow zone.

Figure 7. Increase in trabecular bone in OPG transgenic mice. A-D. Representative photomicrographs of bones from control animals. In A and B, low (4X, 10X) power images of the femurs are shown (Masson Trichrome stain). Stains for tartrate resistant acid phosphatase (TRAP) demonstrate osteoclasts (see arrows) both resorbing cartilage (C) and trabecular bone (D). Note the flattened appearance of osteoclasts on trabecular bone. E-H. Representative photomicrographs of bones from OPG-expressing animals. In E and F, low (4X, 10X) power images of the femurs are shown (Masson Trichrome stain). The clear region is the growth plate cartilage, blue stained area is bone, and the red area is marrow. Note that in contrast to the controls, the trabecular bone has not been resorbed resulting in the absence of the usual marrow cavity. Also, the resulting trabeculae have a variegated appearance with blue and clear areas. The clear areas are remnants of growth plate cartilage that have never been remodelled. Based on TRAP stains, these animals do have osteoclasts (see arrows) at the growth plate (G), which may be reduced in number. However, the surfaces of the trabeculae away from the growth plate are virtually devoid of osteoclasts (H), a finding that stands in direct contrast with the control animals (see D).



Figure 8. HE-OPG expressors do not have a defect in monocyte-macrophage development. One cause for osteopetrosis in mice is defective M-CSF production due to a point mutation in the M-CSF gene. This results in a marked deficit of circulating and tissue based macrophages. The peripheral blood of OPG expressors contained monocytes as assessed by H1E analysis. To affirm the presence of tissue macrophages, immunohistochemistry was performed using F480 antibodies, which recognize a cell surface antigen on murine macrophages. A and C show low power (4X) photomicrographs of the spleens from normal and CR1 overexpressors. Note that both animals have numerous F480 positive cells. Monocyte-macrophages were also present in the marrow of normal (B) and HE-OPG overexpressors (D) (40X).

Figure 9. Structure and sequence of mouse and human OPG cDNA clones. A, B. Mouse cDNA and protein sequence. C, D. Human cDNA and protein sequence. The predicted signal peptides are underlined, and potential sites of N-linked glycosylation are indicated in bold. E, F. Sequence alignment and comparison of rat, mouse and human OPG amino acid sequences.

Figure 10. Comparison of conserved sequences in extracellular domain of TNFR-I and human OPG. PrettyPlot (Wisconsin GCG Package, Version 8.1) of the TNFR1 and OPG alignment described in example 6. Top line, human TNFR1 sequences encoding domains 1-4. Bottom line, human OPG sequences encoding domains 1-4. Conserved residues are highlighted by rectangular boxes.

Figure 11. Three-dimensional representation of human OPG. Side-view of the Molescript display of the predicted 3-dimensional structure of human OPG residues 25 through 163, (wide line), co-crystallized with human



TNF $\beta$  (thin line). As a reference for orientation, the bold arrows along the OPG polypeptide backbone are pointing in the N-terminal to C-terminal direction. The location of individual cysteine residue side chains are inserted along the polypeptide backbone to help demonstrate the separate cysteine-rich domains. The TNF $\beta$  molecule is aligned as described by Banner *et al.* (1993).

Figure 12. Structure of OPG cysteine-rich domains. Alignment of the human (top line SEQ ID NO:136) and mouse (bottom line) OPG amino acid sequences highlighting the predicted domain structure of OPG. The polypeptide is divided into two halves; the N-terminus (A), and C-terminus (B). The N-terminal half is predicted to contain four cysteine rich domains (labeled 1-4). The predicted intrachain disulfide bonds are indicated by bold lines, labeled "SS1", "SS2", or "SS3". Tyrosine 28 and histidine 75 (underlined) are predicted to form an ionic interaction. Those amino acids predicted to interact with an OPG ligand are indicated by bold dots above the appropriate residue. The cysteine residues located in the C-terminal half of OPG are indicated by rectangular boxes.

Figure 13. Expression and secretion of full length and truncated mouse OPG-Fc fusion proteins. A. Map indicating points of fusion to the human IgG1 Fc domain are indicated by arrowheads. B. Silver stain of a SDS-polyacrylamide gel of conditioned media obtained from cells expressing either Fl.Fc (Full length OPG fused to Fc at Leucine 401) or CT.Fc (Carboxy-terminal truncated OPG fused to Fc at threonine 180) fusion protein expression vectors. Lane 1, parent pCEP4 expression vector cell line; Lane 2, Fl.Fc vector cell line; Lane 3, CT.Fc vector cell line. C. Western blot of conditioned media obtained from Fl.Fc and CT.Fc fusion



protein expression vectors probed with anti-human IgG1 Fc domain (Pierce). Lane 1, parent pCEP4 expression vector cell line; Lane 2, Fl.Fc vector cell line; Lane 3, CT.Fc vector cell line.

5        Figure 14. Expression of human OPG in *E. coli*. A. Construction of a bacterial expression vector. The LORF of the human OPG gene was amplified by PCR, then joined to a oligonucleotide linker fragment (top strand is SEQ ID NO:137; bottom strand is SEQ ID NO:127), and ligated  
10 into pAMG21 vector DNA. The resulting vector is capable of expressing OPG residues 32-401 linked to a N-terminal methionine residue. B SDS-PAGE analysis of uninduced and induced bacterial harboring the pAMG21-human OPG -32-401 plasmid. Lane 1, MW standards; lane  
15 2, uninduced bacteria; lane 3, 30°C induction; lane 4, 37°C induction; lane 5, whole cell lysate from 37°C induction; lane 6, soluble fraction of whole cell lysate; lane 7, insoluble fraction of whole cell lysate; lane 8, purified inclusion bodies obtained from  
20 whole cell lysate.

Figure 15. Analysis of recombinant murine OPG produced in CHO cells by SDS-PAGE and western blotting. An equal amount of CHO conditioned media was applied to each lane shown, and was prepared by treatment with  
25 either reducing sample buffer (left lane), or non-reducing sample buffer (right lane). After electrophoresis, the resolved proteins were transferred to a nylon membrane, then probed with anti-OPG antibodies. The relative positions of the 55 kd  
30 monomeric and 100 kd dimeric forms of OPG are indicated by arrowheads.

Figure 16. Pulse-chase analysis of recombinant murine OPG produced in CHO cells. CHO cells were pulse-labeled with <sup>35</sup>S-methionine/cysteine, then chased  
35 for the indicated time. Metabolically labeled cultures were separated into both conditioned media and cells,



and detergent extracts were prepared from each, clarified, then immunoprecipitated with anti-OPG antibodies. The immunoprecipitates were resolved by SDS-PAGE, and exposed to film. Top left and right panels; samples analyzed under non-reducing conditions. Lower left and right panels; samples analyzed under reducing conditions. Top and bottom left panels; Cell extracts. Top and bottom right panels; Conditioned media extracts. The relative mobility of the 55 kd monomeric and 100 kd dimeric forms of OPG are indicated by arrowheads.

Figure 17. Expression of OPG in the CTLL-2 cell line. Serum-free conditioned media from CTLL-2 cells and CHO-mu OPG [1-401] transfected cells was prepared, concentrated, then analyzed by non-reducing SDS-PAGE and western blotting. Left lane; CTLL-2 conditioned media. Right lane; CHO-muOPG conditioned media. The relative mobility of the 55 kd monomeric and 100 kd dimeric forms of OPG are indicated by arrowheads.

Figure 18. Detection of OPG expression in serum samples and liver extracts obtained from control and OPG transgenic mice. Transgenic mice were constructed as described in Example 4. OPG expression was visualized after SDS-PAGE followed by Western blotting using anti-OPG antibodies.

Figure 19. Effects of huOPG [22-401]-Fc fusion protein on osteoclast formation in vitro. The osteoclast forming assay was performed as described in Example 11A in the absence (control) or presence of the indicated amounts of huOPG [22-401]-Fc fusion. Osteoclast formation was visualized by histochemical staining for tartrate acid phosphatase (TRAP). A. OPG added to 100 ng/ml. D. OPG added to 0.1 ng/ml. E. OPG added to 0.01 ng/ml. F. OPG added to 0.001 ng/ml. G. Control. No OPG added.



Figure 20. Decrease in osteoclast culture TRAP activity with increasing amounts of OPG. Indicated concentrations of huOPG [22-401]-Fc fusion protein were added to osteoclast forming assay and TRAP activity  
5 quantitated as described in Example 11A.

Figure 21. Effect of OPG on a terminal stage of osteoclast differentiation. huOPG [22-401]-Fc fusion was added to the osteoclast forming assay during the intermediate stage of osteoclast maturation (days 5-6;  
10 OPG-CTL) or during the terminal stage of osteoclast maturation (days 7-15; CTL-OPG). TRAP activity was quantitated and compared with the activity observed in the absence of OPG (CTL-CTL) in the presence of OPG throughout (OPG-OPG).

15 Figure 22. Effects of IL-1 $\beta$ , IL-1 $\alpha$  and OPG on blood ionized calcium in mice. Levels of blood ionized calcium were monitored after injection of IL-1 $\beta$  alone, IL-1 $\alpha$  alone, IL-1 $\beta$  plus muOPG [22-401]-Fc, IL-1 $\alpha$  plus muOPG [22-401]-Fc, and muOPG [22-401]-Fc alone. Control  
20 mice received injections of phosphate buffered saline (PBS) only. IL-1 $\beta$  experiment shown in A; IL-1 $\alpha$  experiment shown in B.

Figure 23. Effects of OPG on calvarial osteoclasts in control and IL-1-treated mice. Histological methods  
25 for analyzing mice calvarial bone samples are described in Example 11B. Arrows indicate osteoclasts present in day 2-treated mice. Calvarial samples of mice receiving four PBS injections daily (A), one injection of IL-1 and three injections of PBS daily (B), one injection of  
30 PBS and three injections of OPG daily (C), one injection of IL-1 and three injections of OPG daily.

Figure 24. Radiographic analysis of bone accumulation in marrow cavity of normal mice. Mice were injected subcutaneously with saline (A) or muOPG [22-



401]-Fc fusion (5mg/kg/d) for 14 days (B) and bone density determined as described in Example 11C.

Figure 25. Histomorphometric analysis of bone accumulation in marrow cavity of normal mice. Injection experiments and bone histology performed as described in Example 11C.

Figure 26. Histology analysis of bone accumulation in marrow cavity of normal mice. Injection experiments and bone histology performed as described in Example 11C. A. Saline injection B. Injection of muOPG [22-401]-Fc fusion.

Figure 27. Activity of OPG administered to ovariectomized rats. In this two week experiment the trend to reduced bone density appears to be blocked by OPG or other anti-resorptive therapies. DEXA measurements were taken at time of ovariectomy and at week 1 and week 2 of treatment. The results are expressed as % change from the initial bone density (Mean +/- SEM).

Figure 28. Bone density in the femoral metaphysis, measured by histomorphometric methods, tends to be lower in ovariectomized rats (OVX) than sham operated animals (SHAM) 17 days following ovariectomy. This effect was blocked by OPG-Fc, with OPG-Fc treated ovariectomized rats (OVX+OPG) having significantly higher bone density than vehicle treated ovariectomized rats (OVX). (Mean +/- SEM).

Figure 29A through 29G. Sequence of OPG-Fc. DNA and encoded protein sequences are shown. Restriction sites for various nucleases are noted above the DNA sequence.

Figures 30A through 30D. Effects of OPG-Fc during the course of adjuvant arthritis I male Lewis rats. Paws from rats with adjuvant arthritis induced by 0.5mg mycobacteria in oil were analyzed by DEXA for bone mineral density (BMD). Evaluation of BMD, a 29mm X 25mm



box was centered at the calcaneus (expt AdA-14 2/99, Amgen nb#22957 p47-49). \* compared to normal, # compared to vehicle  $P < 0.05$  Mann-Whitney U test.

- Figures 31A and 31B. Combination treatment with
- 5 OPG-Fc and sTNF-RI on Adjuvant Arthritis in Male Lewis Rats. Area under the curve (AUC) for measurement of paw swelling and BMD were measured as described above for Figure 33 and in the examples hereinafter.



### Detailed Description of the Invention

#### OPG proteins

The term "OPG protein" refers collectively to the novel member of the tumor necrosis factor receptor family described hereinafter, variants and truncations thereof that maintain OPG's activity in increasing bone density, and antibodies to OPG ligand that maintain OPG's activity in increasing bone density. An exemplary assay for measuring such activity is shown in figure 6 and the accompanying text. Exemplary OPG proteins are polypeptides comprising the consensus of the rat, mouse and human sequences (figure 9C), OPG-Fc fusions (figures 13, 29), or the rat, mouse or human OPG sequences (figures 2, 9).

OPG was identified as follows. A novel member of the tumor necrosis factor receptor (TNFR) superfamily was identified as an expressed sequence tag (EST) isolated from a fetal rat intestinal cDNA library. The structures of the full-length rat cDNA clones and the corresponding mouse and human cDNA clones were determined as described in Examples 1 and 6. The rat, mouse and human genes are shown in Figures 2B-2C (SEQ ID NO:120), 9A-9B (SEQ ID NO:122), and 9C-9D (SEQ ID NO:124), respectively. All three sequences showed strong similarity to the extracellular domains of TNFR family members. None of the full-length cDNA clones isolated encoded transmembrane and cytoplasmic domains that would be expected for membrane-bound receptors, suggesting that these cDNAs encode soluble, secreted proteins rather than cell surface receptors. A portion of the human gene spanning nucleotides 1200-1353 shown in Figure 9D was deposited in the Genbank database on November 22, 1995 under accession no. 17188769.

The tissue distribution of the rat and human mRNA was determined as described in Example 2. In rat, mRNA expression was detected in kidney, liver, placenta and



heart with the highest expression in the kidney.  
Expression in skeletal muscle and pancreas was also  
detected. In humans, expression was detected in the  
same tissues along with lymph node, thymus, spleen and  
5 appendix.

The rat cDNA was expressed in transgenic mice  
(Example 3) using the liver-specific ApoE promoter  
expression system. Analysis of expressors showed a  
marked increase in bone density, particularly in long  
10 bones (femurs), vertebrae and flat bones (pelvis).  
Histological analysis of stained sections of bone  
showed severe osteopetrosis (see Example 4) indicating  
a marked imbalance between bone formation and  
resorption which has led to a marked accumulation of  
15 bone and cartilage. A decrease in the number of  
trabecular osteoclasts in the bones of OPG expressor  
animals indicate that a significant portion of the  
activity of the TNFR-related protein may be to prevent  
bone resorption, a process mediated by osteoclasts. In  
20 view of the activity in transgenic expressors, the  
TNFR-related proteins described herein are termed OPGs.

Using the rat cDNA sequence, mouse and human cDNA  
clones were isolated (Example 5). Expression of mouse  
OPG in 293 cells and human OPG in E. coli is described  
25 in Examples 7 and 8. Mouse OPG was produced as an Fc  
fusion which was purified by Protein A affinity  
chromatography. Also described in Example 7 is the  
expression of full-length and truncated human and mouse  
OPG polypeptides in CHO and 293 cells either as fusion  
30 polypeptides to the Fc region of human IgG1 or as  
unfused polypeptides. The expression of full-length and  
truncated human and mouse OPGs in E. coli either as Fc  
fusion polypeptides or as unfused polypeptides is  
described in Example 8. Purification of recombinantly  
35 produced mammalian and bacterial OPG is described in  
Example 10.



The biological activity of OPG was determined using an in vitro osteoclast maturation assay, an in vivo model of interleukin-1 (IL-1) induced hypercalcemia, and injection studies of bone density in normal mice (see Example 11). The following OPG recombinant proteins produced in CHO or 293 cells demonstrated activity in the in E. coli osteoclast maturation assay: muOPG [22-185]-Fc, muOPG [22-194]-Fc, muOPG [22-401]Fc, muOPG [22-401], huOPG [22-201]-Fc, huOPG [22-401]-Fc. muOPG [22-180]-Fc produced in CHO cells and huOPG met[32-401] produced in E. coli did not demonstrate activity in the in vitro assay.

OPG from several sources was produced as a dimer and to some extent as a higher multimer. Rat OPG [22-401] produced in transgenic mice, muOPG [22-401] and huOPG [22-401] produced as a recombinant polypeptide in CHO cells, and OPG expressed as a naturally occurring product from a cytotoxic T cell line were predominantly dimers and trimers when analyzed on nonreducing SDS gels (see Example 9). Truncated OPG polypeptides having deletions in the region of amino acids 186-401 (e.g., OPG [1-185] and OPG [1-194]) were predominantly monomeric suggesting that the region 186-401 may be involved in self-association of OPG polypeptides. However, huOPG met[32-401] produced in E. coli was largely monomeric.

OPG may be important in regulating bone resorption. The protein appears to act as a soluble receptor of the TNF family and may prevent a receptor-ligand interaction involved in the osteolytic pathway. One aspect of the regulation appears to be a reduction in the number of osteoclasts.

OPG proteins encompassed by the invention include rat [1-401], rat [22-180], rat [22-401], rat [22-401]-Fc fusion, rat [1-180]-Fc fusion, mouse [1-401], mouse [1-180], mouse [22-401], human [1-401], mouse [22-180],



human [22-401], human [22-180], human [1-180], human [22-180]-Fc fusion and human met-32-401. Amino acid numbering is as shown in SEQ ID NO:121 (rat), SEQ ID NO:123 (mouse) and SEQ ID NO:125 (human). Also

5 encompassed are polypeptide derivatives having deletions or carboxy-terminal truncations of part or all of amino acids residues 180-401 of OPG; one or more amino acid changes in residues 180-401; deletion of part or all of a cysteine-rich domain of OPG, in

10 particular deletion of the distal (carboxy-terminal) cysteine-rich domain; and one or more amino acid changes in a cysteine-rich domain, in particular in the distal (carboxy-terminal) cysteine-rich domain. In one embodiment, OPG has from 1 to about 216 amino acids

15 deleted from the carboxy terminus. In another embodiment, OPG has from 1 to about 10 amino acids deleted from the mature amino terminus (wherein the mature amino terminus is at residue 22) and, optionally, has from 1 to about 216 amino acids deleted

20 from the carboxy terminus.

Additional OPG proteins encompassed by the invention include the following: human [22-180]-Fc fusion, human [22-201]-Fc fusion, human [22-401]-Fc fusion, mouse [22-185]-Fc fusion, mouse [22-194]-Fc

25 fusion. These polypeptides are produced in mammalian host cells, such as CHO or 293 cells, Additional OPG polypeptides encompassed by the invention which are expressed in procaryotic host cells include the following: human met[22-401], Fc-human met[22-401]

30 fusion (Fc region is fused at the amino terminus of the full-length OPG coding sequence as described in Example 8), human met[22-401]-Fc fusion (Fc region fused to the full-length OPG sequence), Fc-mouse met[22-401] fusion, mouse met[22-401]-Fc fusion, human met[27-401], human

35 met[22-185], human met[22-189], human met[22-194], human met[22-194] (P25A), human met [22-194] (P26A),



human met[27-185], human met[27-189], human met[27-194], human met-arg-gly-ser-(his)<sub>6</sub> [22-401], human met-lys [22-401], human met-(lys)<sub>3</sub>-[22-401], human met[22-401]-Fc (P25A), human met[22-401](P25A), human  
5 met[22-401](P26A), human met[22-401] (P26D), mouse met[22-401], mouse met[27-401], mouse met[32-401], mouse met[27-180], mouse met[22-189], mouse met[22-194], mouse met[27-189], mouse met[27-194], mouse met-lys[22-401], mouse HEK[22-401](A45T), mouse met-  
10 lys-(his)<sub>7</sub>[22-401], mouse met-lys[22-401]-(his)<sub>7</sub> and mouse met[27-401] (P33E, G36S, A45P). It is understood that the above OPG polypeptides produced in procaryotic host cells have an amino-terminal methionine residue, if such a residue is not indicated. In specific  
15 examples, OPG-Fc fusion were produced using a 227 amino acid region of human IgG1- $\gamma$ 1 was used having the sequence as shown in Ellison *et al.* (1982) Nuc. Acids Res. 10: 4071-9. However, variants of the Fc region of human IgG may also be used.

20 Analysis of the biological activity of carboxy-terminal OPG truncations fused to the human IgG1 Fc region indicates a portion of OPG of about 164 amino acids which is required for activity. This region encompasses amino acids 22-185, preferably those in  
25 Figure 9C-9D (SEQ ID NO:125), and comprises four cysteine-rich domains characteristic of the cysteine-rich domains of TNFR extraceullular domains. Proteins comprising this 164 amino acid sequence are within the meaning of "OPG protein" in this invention.

30 OPG proteins of the invention also may be isolated and purified from other polypeptides present in tissues, cell lines and transformed host cells expressing OPG, or purified from components in cell cultures containing the secreted protein. In one  
35 embodiment, the polypeptide is free from association



with other human proteins, such as the expression product of a bacterial host cell.

A method for the purification of OPG from natural sources and from transfected host cells is also included. The purification process may employ one or more standard protein purification steps in an appropriate order to obtain purified protein. The chromatography steps can include ion exchange, gel filtration, hydrophobic interaction, reverse phase, chromatofocusing, affinity chromatography employing an anti-OPG antibody or biotin-streptavidin affinity complex and the like.

#### IL-1 inhibitors

One of the most potent inflammatory cytokines yet discovered is interleukin-1 (IL-1). IL-1 is thought to be a key mediator in many diseases and medical conditions. It is manufactured (though not exclusively) by cells of the macrophage/monocyte lineage and may be produced in two forms: IL-1 alpha (IL-1 $\alpha$ ) and IL-1 beta (IL-1 $\beta$ ).

A disease or medical condition is considered to be an "interleukin-1 mediated disease" if the spontaneous or experimental disease or medical condition is associated with elevated levels of IL-1 in bodily fluids or tissue or if cells or tissues taken from the body produce elevated levels of IL-1 in culture. In many cases, such interleukin-1 mediated diseases are also recognized by the following additional two conditions: (1) pathological findings associated with the disease or medical condition can be mimicked experimentally in animals by administration of IL-1 or upregulation of expression of IL-1; and (2) a pathology induced in experimental animal models of the disease or medical condition can be inhibited or abolished by treatment with agents that inhibit the action of IL-1. In most interleukin-1 mediated diseases at least two of



the three conditions are met, and in many interleukin-1 mediated diseases all three conditions are met.

A non-exclusive list of acute and chronic interleukin-1 (IL-1)-mediated diseases includes but is  
5 not limited to the following:

- acute pancreatitis;
- ALS;
- Alzheimer's disease;
- cachexia/anorexia, including AIDS-induced
- 10 cachexia;
- asthma and other pulmonary diseases;
- atherosclerosis;
- autoimmune vasculitis;
- chronic fatigue syndrome;
- 15 Clostridium associated illnesses, including  
Clostridium-associated diarrhea;
- coronary conditions and indications,  
including congestive heart failure, coronary  
restenosis, myocardial infarction, myocardial
- 20 dysfunction (e.g., related to sepsis), and coronary  
artery bypass graft;
- cancer, such as multiple myeloma and  
myelogenous (e.g., AML and CML) and other leukemias, as  
well as tumor metastasis;
- 25 diabetes (e.g., insulin diabetes);
- endometriosis;
- fever;
- fibromyalgia;
- glomerulonephritis;
- 30 graft versus host disease/transplant  
rejection;
- hemorrhagic shock;
- hyperalgesia;
- inflammatory bowel disease;



inflammatory conditions of a joint, including osteoarthritis, psoriatic arthritis and rheumatoid arthritis;

inflammatory eye disease, as may be  
5 associated with, for example, corneal transplant;  
ischemia, including cerebral ischemia (e.g., brain injury as a result of trauma, epilepsy, hemorrhage or stroke, each of which may lead to neurodegeneration);

10 Kawasaki's disease;  
learning impairment;  
lung diseases (e.g., ARDS);  
multiple sclerosis;  
myopathies (e.g., muscle protein metabolism,

15 esp. in sepsis);  
neurotoxicity (e.g., as induced by HIV);  
osteoporosis;

pain, including cancer-related pain;  
Parkinson's disease;

20 periodontal disease;  
pre-term labor;

psoriasis;  
reperfusion injury;  
septic shock;

25 side effects from radiation therapy;  
temporal mandibular joint disease;  
sleep disturbance;  
uveitis;

or an inflammatory condition resulting from  
30 strain, sprain, cartilage damage, trauma, orthopedic surgery, infection or other disease processes.

Interleukin-1 inhibitors may be from any protein capable of specifically preventing activation of cellular receptors to IL-1, which may result from any  
35 number of mechanisms. Such mechanisms include downregulating IL-1 production, binding free IL-1,



interfering with IL-1 binding to its receptor,  
interfering with formation of the IL-1 receptor complex  
(i.e., association of IL-1 receptor with IL-1 receptor  
accessory protein), or interfering with modulation of  
5 IL-1 signaling after binding to its receptor. Classes  
of interleukin-1 inhibitors include:

interleukin-1 receptor antagonists such as IL-1ra,  
as described below;

anti-IL-1 receptor monoclonal antibodies (e.g., EP  
10 623674), the disclosure of which is hereby incorporated  
by reference;

IL-1 binding proteins such as soluble IL-1  
receptors (e.g., U. S. Pat. No. 5,492,888, U. S. Pat.  
No. 5,488,032, and U. S. Pat. No. 5,464,937, U. S. Pat.  
15 No. 5,319,071, and U.S. Pat. No. 5,180,812, the  
disclosures of which are hereby incorporated by  
reference);

anti-IL-1 monoclonal antibodies (e.g., WO 9501997,  
WO 9402627, WO 9006371, U.S.Pat. No. 4,935,343, EP  
20 364778, EP 267611 and EP 220063, the disclosures of  
which are hereby incorporated by reference);

IL-1 receptor accessory proteins and antibodies  
thereto (e.g., WO 96/23067 and WO 99/37773, the  
disclosure of which is hereby incorporated by  
25 reference);

inhibitors of interleukin-1 beta converting enzyme  
(ICE) or caspase I (e.g., WO 99/46248, WO 99/47545, and  
WO 99/47154, the disclosures of which are hereby  
incorporated by reference), which can be used to  
30 inhibit IL-1 beta production and secretion;

interleukin-1beta protease inhibitors;

and other compounds and proteins which block in  
vivo synthesis or extracellular release of IL-1.

Exemplary IL-1 inhibitors are disclosed in the  
35 following references:



US Pat. Nos. 5,747,444; 5,359,032; 5,608,035;  
5,843,905; 5,359,032; 5,866,576; 5,869,660; 5,869,315;  
5,872,095; 5,955,480; 5,965,564;

International (WO) patent applications 98/21957,  
5 96/09323, 91/17184, 96/40907, 98/32733, 98/42325,  
98/44940, 98/47892, 98/56377, 99/03837, 99/06426,  
99/06042, 91/17249, 98/32733, 98/17661, 97/08174,  
95/34326, 99/36426, 99/36415.

European (EP) patent applications 534978 and  
10 894795.

French patent application FR 2762514.

The disclosures of all of the aforementioned references  
are hereby incorporated by reference.

For purposes of the present invention, IL-1ra and  
15 variants and derivatives thereof as discussed  
hereinafter are collectively termed "IL-1ra  
protein(s)". The molecules described in the above  
references and the variants and derivatives thereof  
discussed hereinafter are collectively termed "IL-1  
20 inhibitors."

Interleukin-1 receptor antagonist (IL-1ra) is a  
human protein that acts as a natural inhibitor of  
interleukin-1 and which is a member of the IL-1 family  
member which includes IL-1 $\alpha$  and IL-1 $\beta$ . Preferred  
25 receptor antagonists (including IL-1ra and variants and  
derivatives thereof), as well as methods of making and  
using thereof, are described in U.S. Patent No.  
5,075,222; WO 91/08285; WO 91/17184; AU 9173636;  
WO 92/16221; WO93/21946; WO 94/06457; WO 94/21275;  
30 FR 2706772; WO 94/21235; DE 4219626, WO 94/20517; WO  
96/22793; WO 97/28828; and WO 99/36541, the disclosures  
of which are incorporated herein by reference. The  
proteins include glycosylated as well as non-  
glycosylated IL-1 receptor antagonists.



Specifically, three useful forms of IL-1ra and variants thereof are disclosed and described in the 5,075,222 patent. The first of these, called "IL-1i" in the '222 patent, is characterized as a 22-23 kD molecule on SDS-PAGE with an approximate isoelectric point of 4.8, eluting from a Mono Q FPLC column at around 52 mM NaCl in Tris buffer, pH 7.6. The second, IL-1ra $\beta$ , is characterized as a 22-23 kD protein, eluting from a Mono Q column at 48 mM NaCl. Both IL-1ra $\alpha$  and IL-1ra $\beta$  are glycosylated. The third, IL-1rax, is characterized as a 20 kD protein, eluting from a Mono Q column at 48 mM NaCl, and is non-glycosylated. 5,075,222 patent also discloses methods for isolating the genes responsible for coding the inhibitors, cloning the gene in suitable vectors and cell types, and expressing the gene to produce the inhibitors.

Those skilled in the art understand that many combinations of deletions, insertions and substitutions (individually or collectively "variant(s)") can be made within the amino acid sequences of IL-1ra, provided that the resulting molecule is biologically active (e.g., possesses the ability to inhibit IL-1). See "Variants of Proteins" hereinafter.

#### TNF- $\alpha$ inhibitors

Many diseases and medical conditions are mediated by TNF and are usually categorized as inflammatory conditions. A "TNF-mediated disease" is a spontaneous or experimental disease or medical condition is associated with elevated levels of TNF in bodily fluids or tissue or if cells or tissues taken from the body produce elevated levels of TNF in culture. In many cases, such TNF-mediated diseases may also be recognized by (1) pathological findings associated with the disease or medical condition can be mimicked experimentally in animals by the administration or



- upregulation of expression of TNF or (2) a pathology induced in experimental animal models of the disease or medical condition can be inhibited or abolished by treatment with agents that inhibit the action of TNF. A
- 5 non-exclusive list of acute and chronic TNF-mediated diseases includes but is not limited to the following:
- cachexia/anorexia;
  - cancer (e.g., leukemias);
  - chronic fatigue syndrome;
  - 10 coronary conditions and indications, including congestive heart failure, coronary restenosis, myocardial infarction, myocardial dysfunction (e.g., related to sepsis), and coronary artery bypass graft; depression;
  - 15 diabetes, including juvenile onset Type 1, diabetes mellitus, and insulin resistance (e.g., as associated with obesity); endometriosis, endometritis, and related conditions;
  - 20 fibromyalgia or analgesia; graft versus host rejection; hyperalgesia; inflammatory bowel diseases, including Crohn's disease and Clostridium difficile-associated diarrhea;
  - 25 ischemia, including cerebral ischemia (brain injury as a result of trauma, epilepsy, hemorrhage or stroke, each of which may lead to neurodegeneration); lung diseases (e.g., adult respiratory distress syndrome; asthma, and pulmonary fibrosis);
  - 30 multiple sclerosis; neuroinflammatory diseases; ocular diseases and conditions, including corneal transplant, ocular degeneration and uveitis; pain, including cancer-related pain;
  - 35 pancreatitis; periodontal diseases;



Pityriasis rubra pilaris (PRP);  
prostatitis (bacterial or non-bacterial) and  
related conditions;  
psoriasis and related conditions;  
5 pulmonary fibrosis;  
reperfusion injury;  
rheumatic diseases, including rheumatoid  
arthritis, osteoarthritis, juvenile (rheumatoid)  
arthritis, seronegative polyarthritis, ankylosing  
10 spondylitis, Reiter's syndrome and reactive arthritis,  
Still's disease, psoriatic arthritis, enteropathic  
arthritis, polymyositis, dermatomyositis, scleroderma,  
systemic sclerosis, vasculitis (e.g., Kawasaki's  
disease), cerebral vasculitis, Lyme disease,  
15 staphylococcal-induced ("septic") arthritis, Sjögren's  
syndrome, rheumatic fever, polychondritis and  
polymyalgia rheumatica and giant cell arteritis);  
septic shock;  
side effects from radiation therapy;  
20 systemic lupus erythematosus (SLE);  
temporal mandibular joint disease;  
thyroiditis;  
tissue transplantation or an inflammatory  
condition resulting from strain, sprain, cartilage  
25 damage, trauma, orthopedic surgery, infection (e.g.,  
HIV, Clostridium difficile and related species) or  
other disease process.

TNF- $\alpha$  inhibitors may act by downregulating or  
inhibiting TNF production, binding free TNF,  
30 interfering with TNF binding to its receptor, or  
interfering with modulation of TNF signaling after  
binding to its receptor. The term "TNF- $\alpha$  inhibitor"  
thus includes solubilized TNF receptors, antibodies to  
TNF, antibodies to TNF receptor, inhibitors of TNF- $\alpha$



converting enzyme (TACE), and other molecules that affect TNF activity.

TNF- $\alpha$  inhibitors of various kinds are disclosed in the art, including the following references:

- 5 European patent applications 308 378; 422 339; 393 438; 398 327; 412 486; 418 014, 417 563, 433 900; 464 533; 512 528; 526 905; 568 928; EP 607 776 (use of leflunomide for inhibition of TNF- $\alpha$ ); 663 210; 542 795; 818 439; 664 128; 542 795; 741 707; 874 819 ; 882 714; 10 880 970; 648 783; 731 791; 895 988; 550 376; 882 714; 853 083; 550 376; 943 616; 939 121; 614 984 ; 853 083
- U.S. Patent Nos. 5,136,021; 5,929,117; 5,948,638; 5,807,862; 5,695,953; 5,834,435; 5,817,822; 5,830,742; 5,834,435; 5,851,556; 5,853,977; 5,359,037; 5,512,544; 15 5,695,953; 5,811,261; 5,633,145; 5,863,926; 5,866,616; 5,641,673; 5,869,677; 5,869,511; 5,872,146; 5,854,003; 5,856,161; 5,877,222; 5,877,200; 5,877,151; 5,886,010; 5,869,660; 5,859,207; 5,891,883; 5,877,180; 5,955,480; 5,955,476; 5,955,435; 5,994,351; 5,990,119; 5,952,320; 20 5,962,481;
- International (WO) patent applications 90/13575, 91/03553, 92/01002, 92/13095, 92/16221, 93/07863, 93/21946, 93/19777, 95/34326, 96/28546, 98/27298, 98/30541, 96/38150, 96/38150, 97/18207, 97/15561, 25 97/12902, 96/25861, 96/12735, 96/11209, 98/39326, 98/39316, 98/38859, 98/39315, 98/42659, 98/39329, 98/43959, 98/45268, 98/47863, 96/33172, 96/20926, 97/37974, 97/37973, 97/47599, 96/35711, 98/51665, 98/43946, 95/04045, 98/56377, 97/12244, 99/00364, 30 99/00363, 98/57936, 99/01449, 99/01139, 98/56788, 98/56756, 98/53842, 98/52948, 98/52937, 99/02510, 97/43250, 99/06410, 99/06042, 99/09022, 99/08688, 99/07679, 99/09965, 99/07704, 99/06041, 99/37818, 99/37625, 97/11668, 99/50238, 99/47672, 99/48491;



Japanese (JP) patent applications 10147531,  
10231285, 10259140, and 10130149, 10316570, 11001481,  
and 127,800/1991;

German (DE) application 19731521;

5 British (GB) applications 2 218 101, 2 326 881, 2  
246 569.

The disclosures of all of the aforementioned  
references are hereby incorporated by reference.

For purposes of this invention, the molecules  
10 disclosed in these references and the sTNFRs and  
variants and derivatives of the sTNFRs and the  
molecules disclosed in the references (see below) are  
collectively termed "TNF- $\alpha$  inhibitors."

For example, EP 393 438 and EP 422 339 teach the  
15 amino acid and nucleic acid sequences of a soluble TNF  
receptor type I (also known as sTNFR-I or 30kDa TNF  
inhibitor) and a soluble TNF receptor type II (also  
known as sTNFR-II or 40kDa TNF inhibitor), collectively  
termed "sTNFRs", as well as modified forms thereof  
20 (e.g., fragments, functional derivatives and variants).  
EP 393 438 and EP 422 339 also disclose methods for  
isolating the genes responsible for coding the  
inhibitors, cloning the gene in suitable vectors and  
cell types, and expressing the gene to produce the  
25 inhibitors.

sTNFR-I and sTNFR-II are members of the nerve  
growth factor/TNF receptor superfamily of receptors  
which includes the nerve growth factor receptor (NGF),  
the B cell antigen CD40, 4-1BB, the rat T-cell antigen  
30 MRC OX40, the fas antigen, and the CD27 and CD30  
antigens (Smith *et al.* (1990), *Science*, 248:1019-1023).  
The most conserved feature amongst this group of cell  
surface receptors is the cysteine-rich extracellular  
ligand binding domain, which can be divided into four  
35 repeating motifs of about forty amino acids and which



contains 4-6 cysteine residues at positions which are well conserved (Smith *et al.* (1990), *supra*).

EP 393 438 teaches a 40kDa TNF inhibitor Δ51 and a 40kDa TNF inhibitor Δ53, which are truncated versions of the full-length recombinant 40kDa TNF inhibitor protein wherein 51 or 53 amino acid residues, respectively, at the carboxyl terminus of the mature protein are removed.

PCT Application No. PCT/US97/12244 teaches truncated forms of sTNFR-I and sTNFR-II which do not contain the fourth domain (amino acid residues Thr<sup>127</sup>-Asn<sup>161</sup> of sTNFR-I and amino acid residues Pro<sup>141</sup>-Thr<sup>179</sup> of sTNFR-II); a portion of the third domain (amino acid residues Asn<sup>111</sup>-Cys<sup>126</sup> of sTNFR-I and amino acid residues Pro<sup>123</sup>-Lys<sup>140</sup> of sTNFR-II); and, optionally, which do not contain a portion of the first domain (amino acid residues Asp<sup>1</sup>-Cys<sup>19</sup> of sTNFR-I and amino acid residues Leu<sup>1</sup>-Cys<sup>32</sup> of sTNFR-II). The truncated sTNFRs of the present invention include the proteins represented by the formula R<sub>1</sub>-[Cys<sup>19</sup>-Cys<sup>103</sup>]-R<sub>2</sub> and R<sub>4</sub>-[Cys<sup>32</sup>-Cys<sup>115</sup>]-R<sub>5</sub>. These proteins are truncated forms of sTNFR-I and sTNFR-II, respectively.

By "R<sub>1</sub>-[Cys<sup>19</sup>-Cys<sup>103</sup>]-R<sub>2</sub>" is meant one or more proteins wherein [Cys<sup>19</sup>-Cys<sup>103</sup>] represents residues 19 through 103 of sTNFR-I, the amino acid residue numbering scheme of which is provided in Figure 1 to facilitate the comparison; wherein R<sub>1</sub> represents a methionylated or nonmethionylated amine group of Cys<sup>19</sup> or of amino-terminus amino acid residue(s) selected from any one of Cys<sup>18</sup> to Asp<sup>1</sup> and wherein R<sub>2</sub> represents a carboxy group of Cys<sup>103</sup> or of carboxy-terminal amino acid residues selected from any one of Phe<sup>104</sup> to Leu<sup>110</sup>.

Exemplary truncated sTNFR-I of the present invention include the following molecules (collectively



termed 2.6D sTNFR-I):  $\text{NH}_2\text{-[Asp}^1\text{-Cys}^{105}\text{]-COOH}$  (also referred to as sTNFR-I 2.6D/C105);  $\text{NH}_2\text{-[Asp}^1\text{-Leu}^{108}\text{]-COOH}$  (also referred to as sTNFR-I 2.6D/C106);  $\text{NH}_2\text{-[Asp}^1\text{-Asn}^{105}\text{]-COOH}$  (also referred to as sTNFR-I 2.6D/N105);  $\text{NH}_2\text{-[Tyr}^9\text{-Leu}^{108}\text{]-COOH}$  (also referred to as sTNFR-I 2.3D/d8);  $\text{NH}_2\text{-[Cys}^{19}\text{-Leu}^{108}\text{]-COOH}$  (also referred to as sTNFR-I 2.3D/d18); and  $\text{NH}_2\text{-[Ser}^{16}\text{-Leu}^{108}\text{]-COOH}$  (also referred to as sTNFR-I 2.3D/d15), either methionylated or nonmethionylated, and variants and derivatives thereof.

By " $\text{R}_3\text{-[Cys}^{32}\text{-Cys}^{115}\text{]-R}_4$ " is meant one or more proteins wherein  $\text{[Cys}^{32}\text{-Cys}^{115}\text{]}$  represents residues  $\text{Cys}^{32}$  through  $\text{Cys}^{115}$  of sTNFR-II, the amino acid residue numbering scheme of which is provided in Figure 2 to facilitate the comparison; wherein  $\text{R}_3$  represents a methionylated or nonmethionylated amine group of  $\text{Cys}^{32}$  or of amino-terminus amino acid residue(s) selected from any one of  $\text{Cys}^{31}$  to  $\text{Leu}^1$  and wherein  $\text{R}_4$  represents a carboxy group of  $\text{Cys}^{115}$  or of carboxy-terminal amino acid residue(s) selected from any one of  $\text{Ala}^{116}$  to  $\text{Arg}^{122}$ .



### Serine Protease Inhibitors

Endogenous proteolytic enzymes degrade invading organisms, antigen-antibody complexes, and certain tissue proteins that are no longer necessary or useful.

- 5 Infective agents may introduce additional proteolytic enzymes into the organism. Protease inhibitors regulate both endogenous and invading proteolytic enzymes.

- A large number of naturally occurring protease inhibitors serve to control the endogenous proteases by  
10 limiting their reactions locally and temporally. In addition, the protease inhibitors may inhibit proteases introduced into the body by infective agents. Tissues that are particularly prone to proteolytic attack and infection, e.g. those of the respiratory tract, are  
15 rich in protease inhibitors.

- Protease inhibitors comprise approximately 10% of the human plasma proteins. At least eight inhibitors have been isolated from this source and characterized in the literature. These include alpha 2-macroglobulin  
20 (alpha 2M), alpha 1-protease inhibitor (alpha 1PI), alpha 1-antichymotrypsin (alpha 1Achy), alpha 1-anticollagenase (alpha 1AC), and inter-alpha-trypsin inhibitor (I-alpha-I).

- A disturbance of the protease/protease inhibitor  
25 balance can lead to protease-mediated tissue destruction, including emphysema, arthritis, glomerulonephritis, periodontitis, muscular dystrophy, tumor invasion and various other pathological conditions. In certain situations, e.g. severe  
30 pathological processes such as sepsis or acute leukemia, the amount of free proteolytic enzymes present increases due to the release of enzyme from the secretory cells. In addition, or separately in other situations, a diminished regulating inhibitor capacity



of the organism may also cause alterations in the protease/protease inhibitor balance. An example of such a diminished regulating inhibitor capacity is an alpha 1-protease inhibitor deficiency, which is highly  
5 correlated with the development of pulmonary emphysema.

In organisms where such aberrant conditions are present, serious damage to the organism can occur unless measures can be taken to control the proteolytic enzymes. Therefore, protease inhibitors have been  
10 sought which are capable of being administered to an organism to control the proteolytic enzymes.

One protease that is of particular pharmacological interest is leukocyte elastase. Leukocyte elastase, when released extracellularly, degrades connective  
15 tissue and other valuable proteins. While it is necessary for a normally functioning organism to degrade a certain amount of connective tissue and other proteins, the presence of an excessive amount of leukocyte elastase has been associated with various  
20 pathological states, such as emphysema and rheumatoid arthritis. To counteract the effects of leukocyte elastase when it is present in amounts greater than normal, a protease inhibitor has been sought which is specific for leukocyte elastase. Such a protease  
25 inhibitor would be especially useful if it were capable of being isolated or prepared in a purified form and in sufficient quantities to be pharmaceutically useful

In the past, at least two leukocyte elastase inhibitors have been identified in the literature. One  
30 protein, described in Schiessler et al., "Acid-Stable Inhibitors of Granulocyte Neutral Proteases in Human Mucous Secretions: Biochemistry and Possible Biological Function", in Neutral Proteases of Human



Polymorphonuclear Leucocytes, Havemann et al. (eds), Urban and Schwarzenberg, Inc. (1978), was isolated from human seminal plasma and sputum and was characterized as being approximately 11 Kda in size with tyrosine as the N-terminal amino acid. The literature reports of this protein have only furnished a partial amino acid sequence, but even this partial sequence indicates that this protein varies substantially from the proteins of the present invention. The reports of the sequence of this protein, in combination with the complete amino acid sequence data for proteins of the present invention, indicate to the present inventors that the product sequenced by Schiessler et al. may have been a degraded protein which was not a single-polypeptide chain.

A second protein, isolated in one instance from human plasma, has been named alpha 1-protease inhibitor. Work on this protein has been summarized in a review by Travis and Salvesen, Ann. Rev. Biochem. 52: 655-709 (1983). The reports of the amino acid sequence of this protein indicate that it too differs substantially from the proteins of the present invention.

Trypsin is another protease of particular interest from a pharmacological standpoint. Trypsin is known to initiate degradation of certain soft organ tissue, such as pancreatic tissue, during a variety of acute conditions, such as pancreatitis. A variety of efforts have been directed toward the treatment of these conditions, without marked success, through the use of proteins which it was hoped would inhibit the action of trypsin. Illustrative of such efforts are attempts to use exogenous bovine trypsin inhibitors in treatment of



human pancreatitis. While such techniques have been attempted in Europe, they have not been approved as effective by the U.S. Food and Drug Administration.

Thus, there is a need for a protease inhibitor  
5 effective in neutralizing excess trypsin in a variety of acute and chronic conditions. As was the case with the leukocyte elastase inhibitor discussed above, a trypsin inhibitor would be particularly useful if it could be isolated and prepared in a purified form and  
10 in sufficient quantities to be pharmaceutically useful.

Cathepsin G is another protease present in large quantities in leukocytes. Cathepsin G is known to be capable of degrading in vitro a variety of valuable proteins, including those of the complement pathway  
15 Pancreatic elastase is another protease which may have a role in pancreatitis. Thus, inhibitors for these proteases are also of pharmaceutical value.

Leukocyte elastase, trypsin, cathepsin G and pancreatic elastase are examples of a class of  
20 proteases known as serine proteases, which have elements of common structure and mechanism. Their activity against different substrates and their sensitivity to different inhibitors are believed to result from changes in only a few amino acid residues.  
25 By analogy, it is possible to conceive of a class of serine protease inhibitors, also having common elements of structure and mechanism, in which changes in a relatively few amino acids will result in inhibition of different proteases, and that at least one member of  
30 this class will inhibit every serine protease of the former class.

A particularly preferred serine protease inhibitor is secretory leukocyte protease inhibitor (SLPI) and



fragments and analogues thereof. Also preferred are anti-leukoprotease (ALP), mucous protease inhibitor (MPI), human seminal plasma inhibitor-I (HUSI-I), bronchial mucus inhibitor (BMI), cervical mucus inhibitor (CUSI). These molecules are especially well-suited for use in conditions leading to bone loss because they are preferentially directed to the cartilage. Exemplary serine protease inhibitors are described in the following, each of which is hereby incorporated by reference: U. S. Pat. No. 4,760,130, issued July 26, 1988; U. S. Pat. No. 5,900,400, issued May 4, 1999, which discloses preferred SLPI analogues; and U. S. Pat. No. 5,633,227, issued May 27, 1997, which discloses preferred SLPI fragments. The molecules disclosed in the foregoing references as well as any variants or analogues thereof as described hereinafter are collectively termed "serine protease inhibitors."

#### IL-18 Inhibitors

IL-18 is a pro-inflammatory cytokine of somewhat recent discovery. IL-18 was found to induce interferon- $\gamma$  and was originally named interferon gamma inducing factor (IGIF). IL-1 upregulates IL-18 production, and IL-18 induces production of a number of proinflammatory cytokines, including IL-6 and MMP-1. Dinarello *et al.* (1998), *J. Leukocyte Biol.* 63: 658-64. Caspase I is also critical for IL-18 production. The art also suggested that TNF- $\alpha$  regulates IL-18 production, and it was found that simultaneous inhibition of TNF- $\alpha$  and IL-18 protected against liver toxicity. Faggioni *et al.* (2000), *PNAS* 97: 2367-72.

IL-18 acts *in vivo* through a receptor system reminiscent of the IL-1 system. IL-18 interacts with a cell surface receptor (IL-18R), which interacts with an accessory protein (IL-18RACp). IL-18-mediated signaling proceeds upon formation of the complex of IL-18, IL-



18R, and IL-18RacP. A natural inhibitor for IL-18 is IL-18bp. Although it bears insignificant sequence homology with IL-18R, IL-18bp's act as a "decoy receptors" by binding to IL-18 molecules and preventing  
5 interaction with IL-18 and subsequent IL-18-mediated signaling.

The present invention concerns methods of treatment using IL-18 inhibitors in combination with the other classes of molecules described herein. Such  
10 combination therapy is useful for treating inflammation and autoimmune diseases generally, as well as IL-1 mediated diseases and TNF-mediated diseases as defined hereinabove. In particular, combination therapy using IL-18 inhibitors is useful for treating arthritis  
15 (particularly rheumatoid arthritis), systemic lupus erythematosus (SLE), graft versus host disease (GvHD), hepatitis and sepsis.

A number of classes of IL-18 inhibitors are known in the art, and all are useful in the present  
20 invention. Suitable IL-18 inhibitors include antibodies binding to IL-18; antibodies binding to IL-18R; antibodies binding to IL-18RacP; IL-18bp; IL-18R fragments (e.g., a solubilized extracellular domain of the IL-18 receptor), peptides binding to IL-18 and  
25 preventing its interaction with IL-18R; peptides binding to IL-18R and preventing its interaction with IL-18 or with IL-18RacP; peptides binding to IL-18RacP and preventing its interaction with IL-18R; and small molecules preventing IL-18 production or interaction  
30 between any of IL-18, IL-18R, and IL-18RacP. Any of the foregoing, with the exception of small molecules, may be linked to half-life extending vehicles known in the art. Such vehicles include the Fc domain, polyethylene glycol, and dextran. These vehicles are reviewed in a  
35 patent application entitled, "Modified Peptides as Therapeutic Agents," U.S. Ser. No. 09/428,082, PCT



appl. no. WO 99/25044, which is hereby incorporated by reference in its entirety.

Useful IL-18 inhibitors are described in the following references, which are hereby incorporated by reference: US Pat. No. 5,912,324, issued July 14, 1994; EP 0 962 531, published Dec. 8, 1999; EP 712 931, published Nov. 15, 1994; US Pat. No. 5,914,253, issued July 14, 1994; WO 97/24441, published July 10, 1997; US Pat. No. 6,060,283, issued May 9, 2000; EP 850 952, published Dec. 26, 1996; EP 864 585, published Sep. 16, 1998; WO 98/41232, published Sep. 24, 1998; US Pat. No. 6,054,487, issued April 25, 2000; WO 99/09063, published Aug 14, 1997; WO 99/22760, published Nov. 3, 1997; WO 99/37772, published Jan. 23, 1998; WO 99/37773, published March 20, 1998; EP 0 974 600, published Jan. 26, 2000; WO 00/12555, published Mar. 9, 2000; Japanese patent application JP 111,399/94, published Oct. 31, 1997; Israel patent application IL 121554 A0, published Feb. 8, 1998.

#### 20 Variants of proteins

Those skilled in the art will understand that one may make many molecules derived in sequence from the aforementioned molecules in which amino acids have been deleted ("deletion variants"), inserted ("addition variants"), or substituted ("substitution variants"). Molecules having such substitutions, additions, deletions, or any combination thereof are termed individually or collectively "variant(s)". Such variants should, however, maintain at some level (including a reduced level) the relevant activity of the unmodified or "parent" molecule (e.g., an STNFR variant possesses the ability to bind TNF). Hereinafter, "parent molecule" refers to an unmodified molecule or a variant molecule lacking the particular variation under discussion; for example, when



discussing substitution below, the parent molecule may be a deletion variant.

5 Variants may be rapidly screened to assess their physical properties. It will be appreciated that such variant(s) will demonstrate similar properties to the unmodified molecule, but not necessarily all of the same properties and not necessarily to the same degree as the corresponding parent molecule.

10 There are two principal variables in the construction of amino acid sequence variant(s): the location of the mutation site and the nature of the mutation. In designing variant(s), the location of each mutation site and the nature of each mutation will depend on the biochemical characteristic(s) to be  
15 modified. Each mutation site can be modified individually or in series, e.g., by (1) deleting the target amino acid residue, (2) inserting one or more amino acid residues adjacent to the located site or (3) substituting first with conservative amino acid  
20 choices and, depending upon the results achieved, then with more radical selections.

Amino acid sequence deletions generally range from about 1 to 30 amino acid residues, preferably from about 1 to 20 amino acid residues, more preferably from  
25 about 1 to 10 amino acid residues and most preferably from about 1 to 5 contiguous residues. Amino-terminal, carboxy-terminal and internal intrasequence deletions are contemplated. Deletions within the amino acid sequences of OPG or the STNFRs may be made, for  
30 example, in regions of low homology with the sequences of other members of the NGF/TNF receptor family. In the case of IL-1ra, deletions may be made in regions of low homology in the IL-1 family (which comprises IL-1  $\alpha$ , IL-1  $\beta$ , and IL-1ra). Deletions in areas of substantial  
35 homology with other members of the family will be more



likely to significantly modify the biological activity. Specifically, the sequence similarity among NGF/TNF receptor family members is particularly high in the region corresponding to the first two disulfide loops of domain 1, the whole of domain 2, and the first disulfide loop of domain 3 (Banner et al. (1993), Cell, 73:431-445). The number of total deletions and/or consecutive deletions preferably will be selected so as to preserve the tertiary structure in the affected domain, e.g., cysteine crosslinking.

An amino acid sequence addition may include insertions of an amino- and/or carboxyl-terminal fusion ranging in length from one residue to one hundred or more residues, as well as internal intrasequence insertions of single or multiple amino acid residues. Internal additions may range generally from about 1 to 20 amino acid residues, preferably from about 1 to 10 amino acid residues, more preferably from about 1 to 5 amino acid residues, and most preferably from about 1 to 3 amino acid residues. Additions within the amino acid sequences of OPG or the STNFRs may be made in regions of low homology with the sequences of other members of the NGF/TNF receptor family. Additions within the amino acid sequence of OPG or the STNFRs in areas of substantial homology with the sequences of other members of the NGF/TNF receptor family will be more likely to significantly modify the biological activity. Additions preferably include amino acid sequences derived from the sequences of the NGF/TNF receptor family members.

An amino-terminus addition is contemplated to include the addition of a methionine (for example, as an artifact of the direct expression in bacterial recombinant cell culture). A further example of an amino-terminal addition includes the fusion of a signal sequence to the amino-terminus of a mature molecule in



order to facilitate its secretion from recombinant host cells. Such signal sequences generally will be obtained from and thus be homologous to the intended host cell species. For prokaryotic host cells that do not  
5 recognize and process the native signal sequence of the mature molecule, the signal sequence may be substituted by a prokaryotic signal sequence selected, for example, from the group of the alkaline phosphatase, penicillinase or heat-stable enterotoxin II leader  
10 sequences. For expression in yeast cells the signal sequence may be selected, for example, from the group of the yeast invertase, alpha factor or acid phosphatase leader sequences. For mammalian cell expression, the native signal sequences (see, e.g., EP  
15 393 438 and EP 422 339 for sTNFRs) are satisfactory, although other mammalian signal sequences may be suitable; for example, sequences derived from other NGF/TNF receptor family members.

An example of an amino- or a carboxy-terminus  
20 addition includes chimeric proteins comprising the amino-terminal or carboxy-terminal fusion of the parent molecules with all or part of the constant domain of the heavy or light chain of human immunoglobulin (individually or collectively, ("Fc variant(s)"). Such  
25 chimeric polypeptides are preferred wherein the immunoglobulin portion of each comprises all of the domains except the first domain of the constant region of the heavy chain of human immunoglobulin such as IgG (e.g., IgG1 or IgG3), IgA, IgM or IgE. A skilled  
30 artisan will appreciate that any amino acid of the immunoglobulin portion can be deleted or substituted with one or more amino acids, or one or more amino acids can be added as long as the parent molecule still maintains some level of its relevant activity and the  
35 immunoglobulin portion shows one or more of its characteristic properties.



Another group of variant(s) is amino acid substitution variant(s). These are variant(s) wherein at least one amino acid residue in a parent molecule is removed and a different residue inserted in its place.

5 Substitution variant(s) include allelic variant(s) which are characterized by naturally-occurring nucleotide sequence changes in the species population that may or may not result in an amino acid change. One skilled in the art can use any information known about

10 the binding or active site of the polypeptide in the selection of possible mutation sites.

One method for identifying amino acid residues or regions for mutagenesis of a protein is called "alanine scanning mutagenesis", as described by Cunningham and

15 Wells (1989), Science, 244:1081-1085, the disclosure of which is hereby incorporated by reference. In this method, an amino acid residue or group of target residues is identified (e.g., charged residues such as Arg, Asp, His, Lys and Glu) and replaced by a neutral

20 or negatively-charged amino acid (most preferably alanine or polyalanine) to affect the interaction of the amino acids with the surrounding aqueous environment in or outside the cell. Those domains/residues demonstrating functional sensitivity

25 to the substitutions are then refined by introducing additional or alternate residues at the sites of substitution. Thus, the site for introducing an amino acid sequence modification is predetermined. To optimize the performance of a mutation at a given site,

30 alanine scanning or random mutagenesis may be conducted and the variant(s) may be screened for the optimal combination of desired activity and degree of activity.

The sites of greatest interest for substitutional mutagenesis include sites in which particular amino

35 acid residues within a parent molecule are substantially different from other species or other



family members in terms of side-chain bulk, charge and/or hydrophobicity. Other sites of interest include those in which particular residues of a parent molecule are identical among other species or other family members, as such positions are generally important for the biological activity of a protein.

Other sites of interest include those in which particular residues are similar or identical with proteins with similar structure or activity to the parent molecule. For sTNFR-I, for example, information has been elucidated relevant to sTNFR-I-like molecules (Banner et al. (1993), supra, and Fu et al. (1995), Protein Engineering, 8(12):1233-1241). Residues Tyr<sup>9</sup>, Thr<sup>39</sup>, His<sup>55</sup> in Domain 1, residues Phe<sup>49</sup>, Ser<sup>63</sup>, Asp<sup>82</sup> in Domain 2 and residues Tyr<sup>92</sup> and Ser<sup>107</sup> in Domain 3 have been identified as being potentially important for the stabilization of the structure of Domains 1, 2 and 3, respectively. Residues Pro<sup>12</sup> and His<sup>55</sup> have been identified as potentially interacting with Ser<sup>86</sup>-Tyr<sup>87</sup> on subunit C of TNF- $\alpha$ . Residues Glu<sup>45</sup>-Phe<sup>49</sup> have been identified as being in a loop which potentially interacts with residues Leu<sup>29</sup>-Arg<sup>32</sup> of TNF- $\alpha$  subunit A. Residues Gly<sup>48</sup> has been identified as potentially interacting with Asn<sup>19</sup>-Pro<sup>20</sup> on subunit A of TNF- $\alpha$ . Residue His<sup>58</sup>-Leu<sup>60</sup> have been identified as being in an extended strand conformation and side chain interactions with residues Arg<sup>31</sup>-Ala<sup>33</sup> on subunit A of TNF- $\alpha$  have been potentially identified with residue His<sup>58</sup> of sTNFR-I specifically interacting with residue Arg<sup>31</sup>. Residues Lys<sup>64</sup>-Arg<sup>66</sup> have been identified as being in an extended strand conformation and have been identified as having side chain and main chain



interactions with residues Ala<sup>145</sup>-Glu<sup>146</sup> and residue Glu<sup>46</sup> on subunit A of TNF- $\alpha$ . Residue Met<sup>69</sup> has been identified as potentially interacting with residue Tyr<sup>115</sup> on subunit A of TNF- $\alpha$ . Residues His<sup>94</sup>-Phe<sup>101</sup> have  
5 been identified as forming a loop which interacts with residues Thr<sup>72</sup>-Leu<sup>75</sup> and Asn<sup>137</sup> of subunit C of TNF- $\alpha$ , with residue Trp<sup>96</sup> of sTNFR-I specifically interacting with residues Ser<sup>71</sup>-Thr<sup>72</sup> on subunit C of TNF- $\alpha$ , Leu<sup>100</sup> of sTNFR-I being in close proximity with residue Asn<sup>137</sup>  
10 on subunit C of TNF- $\alpha$  and residue Gln<sup>102</sup> of sTNFR-I specifically interacting with residue Pro<sup>113</sup> on subunit A of TNF- $\alpha$ .

In addition to the cysteines forming the 3 pairs of disulfide bonds within each of the four domains of  
15 the molecule, there are several other conserved residues that contribute to the stabilization of the tertiary fold of each domain.

There are two main classes into which these stabilizing residues fall. The first type contributes  
20 to the shielding of the disulfide bond sulfur atoms from solvent. An example of this residues in domain 3 is Tyr<sup>92</sup>. In domain 4 Phe<sup>133</sup> helps to shield the Cys<sup>128</sup>-Cys<sup>139</sup> disulfide bond. All four domains have either a Tyr or Phe at these same structurally conserved  
25 locations. The second class of stabilizing residues form hydrogen bonds within their respective domains. Within domain 3 Asn<sup>123</sup> and Ser<sup>107</sup> form a hydrogen bond and Ser<sup>107</sup> forms an additional hydrogen bond with Thr<sup>124</sup>. For domain 4 these residues include Asn<sup>144</sup> and  
30 Ser<sup>141</sup>.

In addition there are hydrogen bonds between domain 3 and 4 that are not seen between other domains.



These hydrogens bonds are (1) Asn<sup>105</sup> main-chain oxygen and Asn<sup>137</sup> side-chain nitrogen and (2) Ser<sup>107</sup> side-chain oxygen and Asn<sup>137</sup> main-chain nitrogen.

Another useful tool in identifying sites suitable  
5 for substitution is molecular modeling. One example of this technique is OPG. Using the homology between OPG and the extracellular ligand binding domains of TNF receptor family members, a three-dimensional model of OPG was generated based upon the known crystal  
10 structure of the extracellular domain of TNFR-I (see Example 6). This model was used to identify those residues within OPG which may be important for biological activity. Cysteine residues that are involved in maintaining the structure of the four  
15 cysteine-rich domains were identified. The following disulfide bonds were identified in the model: Domain 1: cys41 to cys54, cys44 to cys62, tyr23 and his 66 may act to stabilize the structure of this domain; Domain 2: cys65 to cys80, cys83 to cys98, cys87 to cys105;  
20 Domain 3: cys107 to cys118, cys124 to cys142; Domain 4: cys145 to cys160, cys166 to cys185. Residues were also identified which were in close proximity to TNF $\beta$  as shown in Figures 11 and 12A-12B. In this model, it is assumed that OPG binds to a corresponding ligand; TNF $\beta$   
25 was used as a model ligand to simulate the interaction of OPG with its ligand. Based upon this modeling, the following residues in OPG may be important for ligand binding: glu34, lys43, pro66 to gln91 (in particular, pro66, his68, tyr69, tyr70, thr71, asp72, ser73, his76, ser77, asp78, glu79, leu81, tyr82, pro85, val86, lys88,  
30 glu90 and gln91), glu153 and ser155.

Alterations in these amino acid residues, either singly or in combination, may alter the biological activity of OPG. For example, changes in specific  
35 cysteine residues may alter the structure of individual



cysteine-rich domains, whereas changes in residues important for ligand binding may affect physical interactions of OPG with ligand. Structural models can aid in identifying analogs which have more desirable  
5 properties, such as enhanced biological activity, greater stability, or greater ease of formulation.

A skilled artisan will appreciate that initially sites should be modified by substitution in a relatively conservative manner. Such conservative  
10 substitutions are shown in Table 1 under the heading of "Preferred Substitutions". If such substitutions result in a change in biological activity, then more substantial changes (Exemplary Substitutions) may be introduced and/or other additions/deletions may be made  
15 and the resulting products screened.



TABLE 1: Amino Acid Substitutions

<u>Original Residue</u>	<u>Preferred Substitutions</u>	<u>Exemplary Substitutions</u>
Ala (A)	Val	Val; Leu; Ile
Arg (R)	Lys	Lys; Gln; Asn
Asn (N)	Gln	Gln; His; Lys; Arg
Asp (D)	Glu	Glu
Cys (C)	Ser	Ser
Gln (Q)	Asn	Asn
Glu (E)	Asp	Asp
Gly (G)	Pro	Pro
His (H)	Arg	Asn; Gln; Lys; Arg
Ile (I)	Leu	Leu; Val; Met; Ala; Phe; norleucine
Leu (L)	Ile	norleucine; Ile; Val; Met; Ala; Phe
Lys (K)	Arg	Arg; Gln; Asn
Met (M)	Leu	Leu; Phe; Ile
Phe (F)	Leu	Leu; Val; Ile; Ala
Pro (P)	Gly	Gly
Ser (S)	Thr	Thr
Thr (T)	Ser	Ser
Trp (W)	Tyr	Tyr
Tyr (Y)	Phe	Trp; Phe; Thr; Ser
Val (V)	Leu	Ile; Leu; Met; Phe; Ala; norleucine

In making such changes, the hydropathic index of amino acids may be considered. The importance of the  
5 hydropathic amino acid index in conferring interactive biological function on a protein is generally understood in the art (Kyte and Doolittle (1982), J.



Mol. Biol., 157:105-131, the disclosure of which is incorporated herein by reference). It is known that certain amino acids may be substituted for other amino acids having a similar hydropathic index or score and  
5 still retain a similar biological activity.

It is also understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity, particularly where the functionally equivalent protein  
10 or peptide thereby created is intended for use in immunological embodiments, as in the present case. U.S. Patent 4,554,101, the disclosure of which is incorporated herein by reference, states that the greatest local average hydrophilicity of a protein, as  
15 governed by the hydrophilicity of its adjacent amino acids, correlates with its immunogenicity and antigenicity, i.e., with a biological property of the protein.

U.S. Patent 4,554,101 also teaches the  
20 identification and preparation of epitopes from primary amino acid sequences on the basis of hydrophilicity. Through the methods disclosed in U.S. Patent 4,554,101 a skilled artisan would be able to identify epitopes, for example, within the amino acid sequence of an  
25 sTNFR. These regions are also referred to as "epitopic core regions". Numerous scientific publications have been devoted to the prediction of secondary structure, and to the identification of epitopes, from analyses of amino acid sequences (Chou and Fasman (1974),  
30 Biochemistry, 13(2):222-245; Chou and Fasman (1974), Biochemistry, 13(2):211-222; Chou and Fasman (1978), Adv. Enzymol. Relat. Areas Mol. Biol., 47:45-148; Chou and Fasman (1978), Ann. Rev. Biochem., 47:251-276 and Chou and Fasman (1979), Biophys. J., 26:367-384, the  
35 disclosures of which are incorporated herein by reference). Moreover, computer programs are currently



available to assist with predicting antigenic portions and epitopic core regions of proteins. Examples include those programs based upon the Jameson-Wolf analysis (Jameson and Wolf (1988), Comput. Appl. Biosci., 4(1):181-186 and Wolf et al. (1988), Comput. Appl. Biosci., 4(1):187-191, the disclosures of which are incorporated herein by reference); the program PepPlot® (Brutlag et al. (1990), CABS, 6:237-245 and Weinberger et al. (1985), Science, 228:740-742, the disclosures of which are incorporated herein by reference); and other programs for protein tertiary structure prediction (Fetrow and Bryant (1993), BIOTECHNOLOGY, 11:479-483, the disclosure of which is incorporated herein by reference).

In contrast, substantial modifications in the functional and/or chemical characteristics of a parent molecule may be accomplished by selecting substitutions that differ significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the relative charge or hydrophobicity of the protein at the target site or (c) the bulk of the side chain. Naturally-occurring residues are divided into groups based on common side chain properties:

- 1) hydrophobic: norleucine, Met, Ala, Val, Leu, Ile;
- 2) neutral hydrophilic: Cys, Ser, Thr;
- 3) acidic: Asp, Glu;
- 4) basic: Asn, Gln, His, Lys, Arg;
- 5) aromatic: Trp, Tyr, Phe; and
- 6) residues that influence chain orientation: Gly, Pro.

Non-conservative substitutions may involve the exchange of a member of one of these groups for



another. For example, substituted residues may be introduced into regions of OPG or the TNFRs that are homologous with other NGF/TNF receptor family members or into non-homologous regions of the protein.

5 A variety of amino acid substitutions or deletions may be made to modify or add N-linked or O-linked glycosylation sites, resulting in a protein with altered glycosylation. The sequence may be modified to add glycosylation sites to or to delete N-linked or O-linked glycosylation sites from the parent molecule. An  
10 asparagine-linked glycosylation recognition site comprises a tripeptide sequence which is specifically recognized by appropriate cellular glycosylation enzymes. These tripeptide sequences are either  
15 Asn-Xaa-Thr or Asn-Xaa-Ser, where Xaa can be any amino acid other than Pro. In the 30 kDa TNF inhibitor, for example, proven or predicted asparagine residues exist at positions 14, 105 and 111.

Specific mutations of the sequences of the parent  
20 molecules may involve substitution of a non-native amino acid at the amino-terminus, carboxy-terminus or at any site of the protein that is modified by the addition of an N-linked or O-linked carbohydrate. Such modifications may be of particular utility in the  
25 addition of an amino acid (e.g., cysteine), which is advantageous for the linking of a water-soluble polymer to form a derivative. For example, WO 92/16221 describes the preparation of TNFR-I muteins, e.g., wherein an asparagine residue at position 105 of the  
30 native human protein is changed to cysteine (c105 TNFR-I).

In a specific embodiment, a variant polypeptide will preferably be substantially homologous to the amino acid of the parent molecule from which it is  
35 derived. The term "substantially homologous" as used herein means a degree of homology that is in excess of



80%, preferably in excess of 90%, more preferably in excess of 95% or most preferably even 99%. The percentage of homology as described herein is calculated as the percentage of amino acid residues found in the smaller of the two sequences which align with identical amino acid residues in the sequence being compared when four gaps in a length of 100 amino acids may be introduced to assist in that alignment, as set forth by Dayhoff (1972), Atlas of Protein Sequence and Structure, 5:124, National Biochemical Research Foundation, Washington, D.C., the disclosure of which is hereby incorporated by reference. Also included within the term "substantially homologous" are variant(s) of parent molecules that may be isolated by cross-reactivity with antibodies to the parent molecule amino acid sequences or whose genes may be isolated through hybridization with the DNA of parent molecules or segments thereof.

#### Polypeptide Derivatives

This invention also comprises chemically modified derivatives of the parent molecule(s) in which the protein is linked to a nonproteinaceous moiety (e.g., a polymer) in order to modify properties. These chemically modified parent molecules are referred to herein as "derivatives". Such derivatives may be prepared by one skilled in the art given the disclosures herein. Conjugates may be prepared using glycosylated, non-glycosylated or de-glycosylated parent molecule(s) and suitable chemical moieties. Typically non-glycosylated parent molecules and water-soluble polymers will be used. Other derivatives encompassed by the invention include post-translational modifications (e.g., N-linked or O-linked carbohydrate chains, processing of N-terminal or C-terminal ends), attachment of chemical moieties to the amino acid backbone, and chemical modifications of N-linked or O-



linked carbohydrate chains. The polypeptides may also be modified with a detectable label, such as an enzymatic, fluorescent, isotopic or affinity label to allow for detection and isolation of the protein..

5       Water-soluble polymers are desirable because the protein to which each is attached will not precipitate in an aqueous environment, such as a physiological environment. Preferably, the polymer will be pharmaceutically acceptable for the preparation of a  
10       therapeutic product or composition. One skilled in the art will be able to select the desired polymer based on such considerations as whether the polymer/protein conjugate will be used therapeutically and, if so, the therapeutic profile of the protein (e.g., duration of  
15       sustained release; resistance to proteolysis; effects, if any; on dosage; biological activity; ease of handling; degree or lack of antigenicity and other known effects of a water-soluble polymer on a therapeutic proteins).

20       Suitable, clinically acceptable, water-soluble polymers include but are not limited to polyethylene glycol (PEG), polyethylene glycol propionaldehyde, copolymers of ethylene glycol/propylene glycol, monomethoxy-polyethylene glycol,  
25       carboxymethylcellulose, dextran, polyvinyl alcohol (PVA), polyvinyl pyrrolidone, poly-1, 3-dioxolane, poly-1,3,6-trioxane, ethylene/maleic anhydride copolymer, poly ( $\beta$ -amino acids) (either homopolymers or random copolymers), poly(n-vinyl  
30       pyrrolidone)polyethylene glycol, polypropylene glycol homopolymers (PPG) and other polyalkylene oxides, polypropylene oxide/ethylene oxide copolymers, polyoxyethylated polyols (POG) (e.g., glycerol) and other polyoxyethylated polyols, polyoxyethylated.  
35       sorbitol, or polyoxyethylated glucose, colonic acids or



other carbohydrate polymers, Ficoll or dextran and mixtures thereof. As used herein, polyethylene glycol is meant to encompass any of the forms that have been used to derivatize other proteins, such as mono-(C1-  
5 C10) alkoxy- or aryloxy-polyethylene glycol. Polyethylene glycol propionaldehyde may have advantages in manufacturing due to its stability in water.

The water-soluble polymers each may be of any molecular weight and may be branched or unbranched.  
10 Generally, the higher the molecular weight or the more branches, the higher the polymer:protein ratio. The water-soluble polymers each typically have an average molecular weight of between about 2 kDa to about 100 kDa (the term "about" indicating that in preparations  
15 of a water-soluble polymer, some molecules will weigh more, some less, than the stated molecular weight). The average molecular weight of each water-soluble polymer preferably is between about 5 kDa and about 40 kDa, more preferably between about 10kDa and about 35  
20 kDa and most preferably between about 15kDa and about 30 kDa.

There are a number of attachment methods available to those skilled in the art, including acylation reactions or alkylation reactions (preferably to  
25 generate an amino-terminal chemically modified protein) with a reactive water-soluble molecule. See, for example, EP 0 401 384; Malik et al. (1992), Exp. Hematol., 20:1028-1035; Francis (1992), Focus on Growth Factors, 3(2):4-10, published by Mediscript, Mountain  
30 Court, Friern Barnet Lane, London N20 0LD, UK; EP 0 154 316; EP 0 401 384; WO 92/16221; WO 95/34326; WO 95/13312; WO 96/11953; WO 96/19459 and WO 96/19459 and the other publications cited herein that relate to pegylation, the disclosures of which are hereby  
35 incorporated by reference.



Pegylation also may be specifically carried out using water-soluble polymers having at least one reactive hydroxy group (e.g. polyethylene glycol). The water-soluble polymer can be reacted with an activating group, thereby forming an "activated linker" useful in modifying various proteins. The activated linkers can be monofunctional, bifunctional, or multifunctional.

Activating groups which can be used to link the water-soluble polymer to two or more proteins include the following: sulfone, maleimide, sulfhydryl, thiol, triflate, tresylate, azidirine, oxirane and 5-pyridyl. Useful reagents having a reactive sulfone group that can be used in the methods include, without limitation, chlorosulfone, vinylsulfone and divinylsulfone. These PEG derivatives are stable against hydrolysis for extended periods in aqueous environments at pHs of about 11 or less, and can form linkages with molecules to form conjugates which are also hydrolytically stable. Useful homobifunctional derivatives are PEG-bis-chlorosulfone and PEG-bis-vinylsulfone (see WO 95/13312).

WO 97/04003, the disclosure of which is hereby incorporated by reference, teaches methods of making sulfone-activated linkers by obtaining a compound having a reactive hydroxyl group and converting the hydroxyl group to a reactive Michael acceptor to form an activated linker, with tetrahydrofuran as the solvent for the conversion. The application also teaches a process for purifying the activated linkers which utilizes hydrophobic interaction chromatography to separate the linkers based on size and end-group functionality.

As an example, chemically modified derivatives of OPG may provide such advantages as increased stability, increased time in circulation, or decreased immunogenicity (see U.S. Patent No. 4,179,337). The



chemical moieties for derivitization may be selected from water-soluble polymers such as polyethylene glycol, ethylene glycol/propylene glycol copolymers, carboxymethylcellulose, dextran, polyvinyl alcohol and  
5 the like. The polypeptides may be modified at random positions within the molecule, or at predetermined positions within the molecule and may include one, two, three or more attached chemical moieties.

One may specifically desire N-terminally  
10 chemically modified protein. Using polyethylene glycol as an illustration of the present compositions, one may select from a variety of polyethylene glycol molecules (by molecular weight, branching, etc.), the proportion of polyethylene glycol molecules to protein (or  
15 peptide) molecules in the reaction mix, the type of pegylation reaction to be performed, and the method of obtaining the selected N-terminally pegylated protein. The method of obtaining the N-terminally pegylated preparation (i.e., separating this moiety from other  
20 monopegylated moieties if necessary) may be by purification of the N-terminally pegylated material from a population of pegylated protein molecules. Selective N-terminal chemical modification may be accomplished by reductive alkylation which exploits  
25 differential reactivity of different types of primary amino groups (lysine versus the N-terminal) available for derivitization in a particular protein. Under the appropriate reaction conditions, substantially selective derivitization of the protein at the N-  
30 terminus with a carbonyl group containing polymer is achieved.

#### Polyvalent Forms

Polyvalent forms, i.e., molecules comprising more than one active moiety, may be constructed. In one  
35 embodiment, an sTNFR variant may possess multiple tumor necrosis factor binding sites for the TNF ligand.



Additionally, the molecule may possess at least one tumor necrosis factor binding site and, depending upon the desired characteristic of polyvalent form, at least one site of another molecule (e.g., a TNF- $\alpha$  inhibitor(s), and an OPG).

Active moieties may be linked using conventional coupling techniques (see WO 92/16221, WO 95/13312 and WO 95/34326, the disclosures of which are hereby incorporated by reference). For example, WO 92/16221 and WO 95/34326 describe the preparation of various dimerized sTNFR-I molecules, e.g., dimerized c105 sTNFR-I. Techniques for formation of polyvalent forms include photochemical crosslinking (e.g., exposure to ultraviolet light), chemical crosslinking (e.g., with bifunctional linker molecules such as polyethylene glycol), and mutagenesis (e.g., introduction of additional cysteine residues).

Polyvalent forms may be constructed by chemically coupling at least one parent molecule and another moiety with any clinically accepted linker (e.g., a water-soluble polymer). In principle, the linker must not impart new immunogenicity. The linker also must not, by virtue of the new amino acid residues, alter the hydrophobicity and charge balance of the structure, which affects its biodistribution and clearance. A variety of chemical crosslinkers may be used depending upon which properties of the protein dimer are desired. For example, crosslinkers may be short and relatively rigid or longer and more flexible, may be biologically reversible, and may provide reduced immunogenicity or longer pharmacokinetic half-life.

In one example, OPG molecules are linked through the amino terminus by a two step synthesis (see Example 12). In the first step, OPG is chemically modified at the amino terminus to introduce a protected thiol,



which after purification is deprotected and used as a point of attachment for site-specific conjugation through a variety of crosslinkers with a second OPG molecule. Amino-terminal crosslinks include, but are not limited to, a disulfide bond, thioether linkages using short-chain, bis-functional aliphatic crosslinkers, and thioether linkages to variable length, bifunctional polyethylene glycol crosslinkers (PEG "dumbbells"). Also encompassed by PEG dumbbell synthesis of OPG dimers is a byproduct of such synthesis, termed a "monobell". An OPG monobell consists of a monomer coupled to a linear bifunctional PEG with a free polymer terminus. Alternatively, OPG may be crosslinked directly through a variety of amine specific homobifunctional crosslinking techniques which include reagents such as: diethylenetriaminepentaacetic dianhydride (DTPA), p-benzoquinone (pBQ) or bis(sulfosuccinimidyl) suberate (BS<sup>3</sup>) as well as others known in the art. It is also possible to thiolate OPG directly with reagents such as iminothiolane in the presence of a variety of bifunctional, thiol specific crosslinkers, such as PEG bismaleimide, and achieve dimerization and/or dumbbells in a one step process.

The water-soluble polymers for this polyvalent form can be, based on the monomers listed herein, homopolymers, random or block copolymers, terpolymers straight chain or branched, substituted or unsubstituted. The polymer can be of any length or molecular weight, but these characteristics can affect the biological properties. Polymer average molecular weights particularly useful for decreasing clearance rates in pharmaceutical applications are in the range of 2,000 to 35,000 daltons. In addition, the length of the polymer can be varied to optimize or confer the desired biological activity.



Alternatively, a bivalent molecule may consist of two tandem repeats of parent molecules separated by a polypeptide linker region. The design of the polypeptide linkers is similar in design to the  
5 insertion of short loop sequences between domains in the de novo design of proteins (Mutter (1988), TIBS, 13:260-265 and Regan and DeGrado (1988), Science, 241:976-978, the disclosures of which are hereby incorporated by reference). Several different linker  
10 constructs have been assembled and shown to be useful for forming single chain antibodies; the most functional linkers vary in size from 12 to 25 amino acids (amino acids having unreactive side groups, e.g., alanine, serine and glycine) which together constitute  
15 a hydrophilic sequence, have a few oppositely charged residues to enhance solubility and are flexible (Whitlow and Filpula (1991), Methods: A Companion to Methods in Enzymology, 2:97-105; and Brigido et al. (1993), J. Immunol., 150:469-479, the disclosures of  
20 which are hereby incorporated by reference). It has been shown that a linker suitable for single chain antibodies is effective to produce a dimeric form of the human sTNFR-II (Neve et al. (1996), Cytokine, 8(5):365-370, the disclosure of which is hereby  
25 incorporated by reference).

Self-associating variants are another example of polyvalent forms. Such self-associating variants may be bound covalently (typically by disulfide bonds) or noncovalently. Analysis of carboxy-terminal deletions  
30 of OPG, for example, suggest that at least a portion of the region 186-401 is involved in association of OPG polypeptides. Substitution of part or all of the region of OPG amino acids 186-401 with an amino acid sequence capable of self-association is also encompassed by the  
35 invention.



Polyvalent forms may also be formed using substitution variants. Parent molecules may be modified to form dimers or multimers by site-directed mutagenesis to create unpaired cysteine residues for  
5 interchain disulfide bond formation.

Additionally, a parent molecule may be chemically coupled to biotin, and the resulting conjugate may then be allowed to bind to avidin, resulting in tetravalent avidin/biotin/parent molecules. A parent molecule may  
10 also be covalently coupled to dinitrophenol (DNP) or trinitrophenol (TNP) and the resulting conjugates precipitated with anti-DNP or anti-TNP-IgM to form decameric conjugates.

In yet another embodiment, recombinant fusion  
15 proteins may also be produced wherein each recombinant chimeric molecule has a parent molecule(s) sequence amino-terminally or carboxy-terminally fused to all or part of the constant domains, but at least one constant domain, of the heavy or light chain of human  
20 immunoglobulin. For example, a chimeric TNF- $\alpha$  inhibitor(s)/IgG1 (or IgG1/TNF- $\alpha$  inhibitor(s)) fusion protein may be produced from a light chain-containing chimeric gene: a TNF- $\alpha$  inhibitor(s)/human kappa light chain chimera (TNF- $\alpha$  inhibitor(s)/Ck) or a human kappa  
25 light chain/TNF- $\alpha$  inhibitor(s) chimera (Ck/TNF- $\alpha$  inhibitor(s)); or a heavy chain-containing chimeric gene: a TNF- $\alpha$  inhibitor(s)/human gamma-1 heavy chain chimera (TNF- $\alpha$  inhibitor(s)/Cg-1) or a human gamma-1 heavy chain/TNF- $\alpha$  inhibitor(s) chimera (Cg-1/TNF- $\alpha$   
30 inhibitor(s)). Alternatively, an OPG-Fc chimera may be formed as described in WO 97/23614, which is hereby incorporated by reference. Following transcription and translation of a heavy-chain chimeric gene, or of a light chain-containing gene and a heavy-chain chimeric



gene, the gene products may be assembled into a single chimeric molecule having a parent molecule(s) displayed bivalently. Additional details relating to the construction of such chimeric molecules are disclosed  
5 in United States Patent 5,116,964, WO 89/09622, WO 91/16437, WO 97/23614 and EP 315062, the disclosures of which are hereby incorporated by reference.

In yet a further embodiment, recombinant fusion proteins may also be produced wherein each recombinant  
10 chimeric molecule has at least one TNF- $\alpha$  inhibitor(s), as described herein, and at least a portion of the region 186-401 of osteoprotegerin or a variant thereof, as described in European Patent Application No. 96309363.8, the disclosures of which are hereby  
15 incorporated by reference. Either the TNF- $\alpha$  inhibitor(s) or the portion of osteoprotegerin may be at the amino-terminus or the carboxy-terminus of the chimeric molecule.

#### Nucleic Acids

20 The invention provides for an isolated nucleic acid encoding a polypeptide having at least one of the biological activities of OPG. As described herein, the biological activities of OPG include, but are not limited to, any activity involving bone metabolism and  
25 in particular, include increasing bone density. The nucleic acids of the invention are selected from the following:

- a) the nucleic acid sequences as shown in Figures 2B-2C (SEQ ID NO:120), 9A-9B (SEQ ID NO:122), and 9C-9D  
30 (SEQ ID NO:124) or complementary strands thereof;
- b) the nucleic acids which hybridize under stringent conditions with the polypeptide-encoding region in Figures 2B-2C (SEQ ID NO:120), 9A-9B (SEQ ID NO:122), and 9C-9D (SEQ ID NO:124); and



c) nucleic acids which hybridize under stringent conditions with nucleotides 148 through 337 inclusive as shown in Figure 1A.

d) the nucleic acid sequences which are degenerate to the sequences in (a) and (b).

The invention provides for nucleic acids which encode rat, mouse and human OPG as well as nucleic acid sequences hybridizing thereto which encode a polypeptide having at least one of the biological activities of OPG. Also provided for are nucleic acids which hybridize to a rat OPG EST encompassing nucleotides 148-337 as shown in Figure 1A. The conditions for hybridization are generally of high stringency such as 5xSSC, 50% formamide and 42°C described in Example 1 of the specification. Equivalent stringency to these conditions may be readily obtained by adjusting salt and organic solvent concentrations and temperature. The nucleic acids in (b) encompass sequences encoding OPG-related polypeptides which do not undergo detectable hybridization with other known members of the TNF receptor superfamily. In a preferred embodiment, the nucleic acids are as shown in Figures 2B-2C (SEQ ID NO:120), 9A-9B (SEQ ID NO:122), and 9C-9D (SEQ ID NO:124).

The length of hybridizing nucleic acids of the invention may be variable since hybridization may occur in part or all of the polypeptide-encoding regions as shown in Figures 2B-2C (SEQ ID NO:120), 9A-9B (SEQ ID NO:122), and 9C-9D (SEQ ID NO:124), and may also occur in adjacent noncoding regions. Therefore, hybridizing nucleic acids may be truncations or extensions of the sequences shown in Figures 2B-2C (SEQ ID NO:120), 9A-9B (SEQ ID NO:122), and 9C-9D (SEQ ID NO:124). Truncated or extended nucleic acids are encompassed by the invention provided they retain one or more of the biological properties of OPG. The hybridizing nucleic



acids may also include adjacent noncoding regions which are 5' and/or 3' to the OPG coding region. The noncoding regions include regulatory regions involved in OPG expression, such as promoters, enhance,  
5 translational initiation sites, transcription termination sites and the like.

Hybridization conditions for nucleic acids are described in Sambrook et al., Molecular Cloning: A Laboratory Manual, 2<sup>nd</sup> ed. Cold Spring Harbor Laboratory  
10 Press, Cold Spring Harbor, New York (1989)

DNA encoding rat OPG was provided in plasmid pMO-B1.1 deposited with the American Type Culture Collection, Rockville, MD on December 27, 1995 under ATCC accession no. 69970. DNA encoding mouse OPG was  
15 provided in plasmid pRCCMV-murine OPG deposited with the American Type Culture Collection, Rockville, MD on December 27, 1995 under accession no. 69971. DNA encoding human OPG was provided in plasmid pRCCMV -  
human OPG deposited with the American Type Culture  
20 Collection, Rockville, MD on December 27, 1995 under accession no. 69969. The nucleic acids of the invention will hybridize under stringent conditions to the DNA inserts of ATCC accession nos. 69969, 69970, and 69971 and have at least one of the biological activities of  
25 OPG.

Also provided by the invention are derivatives of the nucleic acid sequences as shown in Figures 2B, 9A and 9B. As used herein, derivatives include nucleic acid sequences having addition, substitution, insertion  
30 or deletion of one or more residues such that the resulting sequences encode polypeptides having one or more amino acid residues which have been added, deleted, inserted or substituted and the resulting polypeptide has the activity of OPG. The nucleic acid  
35 derivatives may be naturally occurring, such as by splice variation or polymorphism, or may be constructed



using site-directed mutagenesis techniques available to the skilled worker. One example of a naturally occurring variant of OPG is a nucleic acid encoding a lys to asn change at residue 3 within the leader sequence (see Example 5). It is anticipated that nucleic acid derivatives will encode amino acid changes in regions of the molecule which are least likely to disrupt biological activity. Other derivatives include a nucleic acid encoding a membrane-bound form of OPG having an extracellular domain as shown in Figures 2B-2C (SEQ ID NO:120), 9A-9B (SEQ ID NO:122), and 9C-9D (SEQ ID NO:124) along with transmembrane and cytoplasmic domains.

In one embodiment, derivatives of OPG include nucleic acids encoding truncated forms of OPG having one or more amino acids deleted from the carboxy terminus. Nucleic acids encoding OPG may have from 1 to 216 amino acids deleted from the carboxy terminus. Optionally, an antibody Fc region may extend from the new carboxy terminus to yield a biologically active OPG-Fc fusion polypeptide. (see Example 11). In preferred embodiments, nucleic acids encode OPG having the amino acid sequence from residues 22-185, 22-189, 22-194 or 22-201 (using numbering in Figure 9E-F) and optionally, encoding an Fc region of human IgG.

Also included are nucleic acids encoding truncated forms of OPG having one or more amino acids deleted from the amino terminus. Truncated forms include those lacking part or all the 21 amino acids comprising the leader sequence. Additionally, the invention provides for nucleic acids encoding OPG having from 1 to 10 amino acids deleted from the mature amino terminus (at residue 22) and, optionally, having from 1 to 216 amino acids deleted from the carboxy terminus (at residue 401). Optionally, the nucleic acids may encode a methionine residue at the amino terminus. Examples of



such OPG truncated polypeptides are described in Example 8.

Examples of the nucleic acids of the invention include cDNA, genomic DNA, synthetic DNA and RNA. cDNA is obtained from libraries prepared from mRNA isolated from various tissues expressing OPG. In humans, tissue sources for OPG include kidney, liver, placenta and heart. Genomic DNA encoding OPG is obtained from genomic libraries which are commercially available from a variety of species. Synthetic DNA is obtained by chemical synthesis of overlapping oligonucleotide fragments followed by assembly of the fragments to reconstitute part or all of the coding region and flanking sequences (see U.S. Patent No. 4,695,623 describing the chemical synthesis of interferon genes). RNA is obtained most easily by procaryotic expression vectors which direct high-level synthesis of mRNA, such as vectors using T7 promoters and RNA polymerase.

Nucleic acid sequences of the invention are used for the detection of OPG sequences in biological samples in order to determine which cells and tissues are expressing OPG mRNA. The sequences may also be used to screen cDNA and genomic libraries for sequences related to OPG. Such screening is well within the capabilities of one skilled in the art using appropriate hybridization conditions to detect homologous sequences. The nucleic acids are also useful for modulating the expression of OPG levels by anti-sense therapy or gene therapy. The nucleic acids are also used for the development of transgenic animals which may be used for the production of the polypeptide and for the study of biological activity (see Example 3).

#### Vectors and Host Cells

Expression vectors containing nucleic acid sequences encoding OPG, host cells transformed with



said vectors and methods for the production of OPG are also provided by the invention. An overview of expression of recombinant proteins is found in Methods of Enzymology v. 185, Goeddel, D.V. ed. Academic Press  
5 (1990).

Host cells for the production of OPG include procaryotic host cells, such as E. coli, yeast, plant, insect and mammalian host cells. E. coli strains such as HB101 or JM101 are suitable for expression.  
10 Preferred mammalian host cells include COS, CHOD-, 293, CV-1, 3T3, baby hamster kidney (BHK) cells and others. Mammalian host cells are preferred when post-translational modifications, such as glycosylation and polypeptide processing, are important for OPG activity.  
15 Mammalian expression allows for the production of secreted polypeptides which may be recovered from the growth medium.

Vectors for the expression of OPG contain at a minimum sequences required for vector propagation and  
20 for expression of the cloned insert. These sequences include a replication origin, selection marker, promoter, ribosome binding site, enhancer sequences, RNA splice sites and transcription termination site. Vectors suitable for expression in the aforementioned  
25 host cells are readily available and the nucleic acids of the invention are inserted into the vectors using standard recombinant DNA techniques. Vectors for tissue-specific expression of OPG are also included. Such vectors include promoters which function  
30 specifically in liver, kidney or other organs for production in mice, and viral vectors for the expression of OPG in targeted human cells.

Using an appropriate host-vector system, OPG is produced recombinantly by culturing a host cell  
35 transformed with an expression vector containing nucleic acid sequences encoding OPG under conditions



such that OPG is produced, and isolating the product of expression. OPG is produced in the supernatant of transfected mammalian cells or in inclusion bodies of transformed bacterial host cells. OPG so produced may  
5 be purified by procedures known to one skilled in the art as described below. The expression of OPG in mammalian and bacterial host systems is described in Examples 7 and 8. Expression vectors for mammalian hosts are exemplified by plasmids such as pDSR $\alpha$   
10 described in PCT Application No. 90/14363. Expression vectors for bacterial host cells are exemplified by plasmids pAMG21 and pAMG22-His described in Example 8. Plasmid pAMG21 was deposited with the American Type Culture Collection, Rockville, MD on July 24, 1996  
15 under accession no. 98113. Plasmid pAMG22-His was deposited with the American Type Culture Collection, Rockville, MD on July 24, 1996 under accession no. 98112. It is anticipated that the specific plasmids and host cells described are for illustrative purposes and  
20 that other available plasmids and host cells could also be used to express the polypeptides.

The invention also provides for expression of OPG from endogenous nucleic acids by in vivo or ex vivo recombination events to allow modulation of OPG from  
25 the host chromosome. Expression of OPG by the introduction of exogenous regulatory sequences (e.g. promoters or enhancers) capable of directing the production of OPG from endogenous OPG coding regions is also encompassed. Stimulation of endogenous regulatory  
30 sequences capable of directing OPG production (e.g. by exposure to transcriptional enhancing factors) is also provided by the invention.

#### Antibodies

Also encompassed by the invention are antibodies  
35 specifically binding to OPG. Antigens for the generation of antibodies may be full-length



polypeptides or peptides spanning a portion of the OPG sequence. Immunological procedures for the generation of polyclonal or monoclonal antibodies reactive with OPG are known to one skilled in the art (see, for  
5 example, Harlow and Lane, Antibodies: A Laboratory Manual Cold Spring Harbor Laboratory Press, Cold Spring Harbor N.Y. (1988)). Antibodies so produced are characterized for binding specificity and epitope  
10 recognition using standard enzyme-linked immunosorbent assays. Antibodies also include chimeric antibodies having variable and constant domain regions derived from different species. In one embodiment, the chimeric antibodies are humanized antibodies having murine  
15 variable domains and human constant domains. Also encompassed are complementary determining regions grafted to a human framework (so-called CDR-grafted antibodies). Chimeric and CDR-grafted antibodies are made by recombinant methods known to one skilled in the art. Also encompassed are human antibodies made in  
20 mice.

Anti-OPG antibodies of the invention may be used as an affinity reagent to purify OPG from biological samples (see Example 10). In one method, the antibody is immobilized on CnBr-activated Sepharose and a column  
25 of antibody-Sepharose conjugate is used to remove OPG from liquid samples. Antibodies are also used as diagnostic reagents to detect and quantitate OPG in biological samples by methods described below.

#### Pharmaceutical compositions

30 The invention also provides for pharmaceutical compositions comprising a therapeutically effective amount of a polypeptide comprising OPG or the other therapeutic molecules used (e.g., IL-1ra, sTNF-RI, or SLPI) together with a pharmaceutically acceptable  
35 diluent, carrier, solubilizer, emulsifier, preservative and/or adjuvant. Two or more of the therapeutic



molecules (e.g., OPG, IL-1ra, sTNF-RI, or SLPI) can be formulated together or packaged together in a kit. The term "therapeutically effective amount" means an amount which provides a therapeutic effect for a specified  
5 condition and route of administration. The composition may be in a liquid or lyophilized form and comprises a diluent (Tris, acetate or phosphate buffers) having various pH values and ionic strengths, solubilizer such as Tween or Polysorbate, carriers such as human serum  
10 albumin or gelatin, preservatives such as thimerosal or benzyl alcohol, and antioxidants such as ascorbic acid or sodium metabisulfite. Also encompassed are compositions comprising any of the therapeutic molecules modified with water-soluble polymers to  
15 increase solubility or stability. Compositions may also comprise incorporation of any of the therapeutic molecules into liposomes, microemulsions, micelles or vesicles for controlled delivery over an extended period of time.

20 Specifically, compositions herein may comprise incorporation into polymer matrices such as hydrogels, silicones, polyethylenes, ethylene-vinyl acetate copolymers, or biodegradable polymers. Examples of hydrogels include polyhydroxyalkylmethacrylates (p-  
25 HEMA), polyacrylamide, polymethacrylamide, polyvinylpyrrolidone, polyvinyl alcohol and various polyelectrolyte complexes. Examples of biodegradable polymers include polylactic acid (PLA), polyglycolic acid (PGA), copolymers of PLA and PGA, polyamides and  
30 copolymers of polyamides and polyesters. Other controlled release formulations include microcapsules, microspheres, macromolecular complexes and polymeric beads which may be administered by injection.

35 Selection of a particular composition will depend upon a number of factors, including the condition being treated, the route of administration and the



pharmacokinetic parameters desired. A more extensive survey of component suitable for pharmaceutical compositions is found in Remington's Pharmaceutical Sciences, 18<sup>th</sup> ed. A.R. Gennaro, ed. Mack, Easton, PA  
5 (1980).

Compositions of the invention may be administered by injection, either subcutaneous, intravenous or intramuscular, or by oral, nasal, pulmonary or rectal administration. The route of administration eventually  
10 chosen will depend upon a number of factors and may be ascertained by one skilled in the art.

The invention also provides for pharmaceutical compositions comprising a therapeutically effective amount of the nucleic acids of the invention together  
15 with a pharmaceutically acceptable adjuvant. Nucleic acid compositions will be suitable for the delivery of part or all of the therapeutic molecule coding region to cells and tissues as part of an anti-sense or gene therapy regimen.

## 20 Methods of Treatment

Bone tissue provides support for the body and consists of mineral (largely calcium and phosphorous), a matrix of collagenous and noncollagenous proteins, and cells. Three types of cells found in bone,  
25 osteocytes, osteoblasts and osteoclasts, are involved in the dynamic process by which bone is continually formed and resorbed. Osteoblasts promote formation of bone tissue whereas osteoclasts are associated with resorption. Resorption, or the dissolution of bone  
30 matrix and mineral, is a fast and efficient process compared to bone formation and can release large amounts of mineral from bone. Osteoclasts are involved in the regulation of the normal remodeling of skeletal tissue and in resorption induced by hormones. For  
35 instance, resorption is stimulated by the secretion of parathyroid hormone in response to decreasing



concentrations of calcium ion in extracellular fluids. In contrast, inhibition of resorption is the principal function of calcitonin. In addition, metabolites of vitamin D alter the responsiveness of bone to parathyroid hormone and calcitonin.

After skeletal maturity, the amount of bone in the skeleton reflects the balance (or imbalance) of bone formation and bone resorption. Peak bone mass occurs after skeletal maturity prior to the fourth decade. Between the fourth and fifth decades, the equilibrium shifts and bone resorption dominates. The inevitable decrease in bone mass with advancing years starts earlier in females than males and is distinctly accelerated after menopause in some females (principally those of Caucasian and Asian descent).

Osteopenia is a condition relating generally to any decrease in bone mass to below normal levels. Such a condition may arise from a decrease in the rate of bone synthesis or an increase in the rate of bone destruction or both. The most common form of osteopenia is primary osteoporosis, also referred to as postmenopausal and senile osteoporosis. This form of osteoporosis is a consequence of the universal loss of bone with age and is usually a result of increase in bone resorption with a normal rate of bone formation. About 25 to 30 percent of all white females in the United States develop symptomatic osteoporosis. A direct relationship exists between osteoporosis and the incidence of hip, femoral, neck and inter-trochanteric fracture in women 45 years and older. Elderly males develop symptomatic osteoporosis between the ages of 50 and 70, but the disease primarily affects females.

The cause of postmenopausal and senile osteoporosis is unknown. Several factors have been identified which may contribute to the condition. They include alteration in hormone levels accompanying aging



and inadequate calcium consumption attributed to decreased intestinal absorption of calcium and other minerals. Treatments have usually included hormone therapy or dietary supplements in an attempt to retard  
5 the process. To date, however, an effective treatment for bone loss does not exist.

The invention provides for a method of treating a bone disorder using a therapeutically effective amount of OPG. The bone disorder may be any disorder  
10 characterized by a net bone loss (osteopenia or osteolysis). In general, treatment with OPG is anticipated when it is necessary to suppress the rate of bone resorption. Thus treatment may be done to reduce the rate of bone resorption where the resorption  
15 rate is above normal or to reduce bone resorption to below normal levels in order to compensate for below normal levels of bone formation.

Conditions which are treatable with OPG include the following:

- 20 • Osteoporosis, such as primary osteoporosis, endocrine osteoporosis (hyperthyroidism, hyperparathyroidism, Cushing's syndrome, and acromegaly), hereditary and congenital forms of osteoporosis (osteogenesis imperfecta,  
25 homocystinuria, Menkes' syndrome, and Riley-Day syndrome) and osteoporosis due to immobilization of extremities.
- Paget's disease of bone (osteitis deformans) in adults and juveniles
- 30 • Osteomyelitis, or an infectious lesion in bone, leading to bone loss.
- Hypercalcemia resulting from solid tumors (breast, lung and kidney) and hematologic malignancies (multiple myeloma, lymphoma and leukemia),  
35 idiopathic hypercalcemia, and hypercalcemia



associated with hyperthyroidism and renal function disorders.

- Osteopenia following surgery, induced by steroid administration, and associated with disorders of the small and large intestine and with chronic hepatic and renal diseases.
- Osteonecrosis, or bone cell death, associated with traumatic injury or nontraumatic necrosis associated with Gaucher's disease, sickle cell anemia, systemic lupus erythematosus, rheumatoid arthritis, periodontal disease, osteolytic metastasis, and other conditions

It is understood that OPG may be used alone or in conjunction with other factors for the treatment of bone disorders. In one embodiment, osteoprotegerin is used in conjunction with a therapeutically effective amount of a factor which stimulates bone formation. Such factors include but are not limited to the bone morphogenic factors designated BMP-1 through BMP-12; transforming growth factor- $\beta$  (TGF- $\beta$ ) and TGF- $\beta$  family members; interleukin-1 (IL-1) inhibitors; TNF $\alpha$  inhibitors; parathyroid hormone and analogs thereof, parathyroid related protein and analogs thereof; E series prostaglandins; bisphosphonates (such as alendronate and others); bone-enhancing minerals such as fluoride and calcium; non-steroidal anti-inflammatory drugs (NSAIDs), including COX-2 inhibitors, such as Celebrex<sup>™</sup> and Vioxx<sup>™</sup>; immunosuppressants, such as methotrexate or leflunomide; serine protease inhibitors such as secretory leukocyte protease inhibitor (SLPI); IL-6 inhibitors (e.g., antibodies to IL-6), IL-8 inhibitors (e.g., antibodies to IL-8); IL-18 inhibitors (e.g., IL-18 binding protein or IL-18 antibodies); Interleukin-1 converting enzyme (ICE) modulators; fibroblast growth



factors FGF-1 to FGF-10 and FGF modulators; PAF antagonists; keratinocyte growth factor (KGF), KGF-related molecules, or KGF modulators; matrix metalloproteinase (MMP) modulators; Nitric oxide  
5 synthase (NOS) modulators, including modulators of inducible NOS; modulators of glucocorticoid receptor; modulators of glutamate receptor; modulators of lipopolysaccharide (LPS) levels; and noradrenaline and modulators and mimetics thereof.

10 The invention also relates to treatment of IL-1 mediated disease by treatment with an IL-1 inhibitor in conjunction with a serine protease inhibitor. In particular, this method is useful for treatment of asthma and rheumatoid arthritis.

15 The invention relates further to treatment of TNF-mediated disease by treatment with a TNF inhibitor in conjunction with a serine protease inhibitor. In particular, this method is useful for treatment of rheumatoid arthritis.

20 In preferred embodiments, a polypeptide comprising OPG is used in conjunction with particular therapeutic molecules to treat various inflammatory conditions, autoimmune conditions, and other conditions leading to bone loss. Depending on the condition and the desired  
25 level of treatment, two, three, or more agents may be administered. These agents may be provided together by inclusion in the same formulation or inclusion in a treatment kit, or they may be provided separately. When administered by gene therapy, the genes encoding the  
30 protein agents may be included in the same vector, optionally under the control of the same promoter region, or in separate vectors. Particularly preferred molecules in the aforementioned classes are as follows.



- IL-1 inhibitors: IL-1ra proteins and soluble IL-1 receptors. The most preferred IL-1 inhibitor is anakinra.
- TNF- $\alpha$  inhibitors: soluble tumor necrosis factor receptor type I (sTNF-RI; -RI is also called the p55 receptor); soluble tumor necrosis factor receptor type II (also called the p75 receptor); and monoclonal antibodies that bind the TNF receptor. Most preferred is sTNF-RI as described in WO 98/24463, etanercept (Enbrel<sup>®</sup>), and Avakine<sup>®</sup>. Exemplary TNF- $\alpha$  inhibitors are described in EP 422 339, EP 308 378, EP 393 438, EP 398 327, and EP 418 014.
- serine protease inhibitors: SLPI, ALP, MPI, HUSI-I, BMI, and CUSI. These inhibitors also may be viewed as exemplary LPS modulators, as SLPI has been shown to inhibit LPS responses. Jin *et al.* (1997), *Cell* 88(3): 417-26 (incorporated by reference).

Particularly preferred methods of treatment concern use of TNF- $\alpha$  inhibitors and IL-1 inhibitors in conjunction with polypeptides comprising OPG. Such polypeptides may be used with either or both TNF- $\alpha$  inhibitors and IL-1 inhibitors for treatment of conditions such as rheumatoid arthritis and multiple sclerosis.

The following examples are offered to more fully illustrate the invention, but are not construed as limiting the scope thereof.

30

#### EXAMPLE 1

##### Identification and isolation of the rat OPG cDNA

Materials and methods for cDNA cloning and analysis are described in Maniatis *et al.*, *ibid.* Polymerase chain reactions (PCR) were performed using a Perkin-Elmer 9600 thermocycler using PCR reaction mixture (Boehringer-Mannheim) and primer concentrations



specified by the manufacturer. In general, 25-50  $\mu$ l reactions were denatured at 94°C, followed by 20-40 cycles of 94°C for 5 seconds, 50-60°C for 5 seconds, and 72°C for 3-5 minutes. Reactions were then treated for 72 °C for 3-5 minutes. Reactions were then analyzed by gel electrophoresis as described in Maniatis et al., ibid.

A cDNA library was constructed using mRNA isolated from embryonic d20 intestine for EST analysis (Adams et al. Science 252, 1651-1656 (1991)). Rat embryos were dissected, and the entire developing small and large intestine removed and washed in PBS. Total cell RNA was purified by acid guanidinium thiocyanate-phenol-chloroform extraction (Chomczynski and Sacchi Anal. Biochem. 162, 156-159, (1987)). The poly (A+) mRNA fraction was obtained from the total RNA preparation by adsorption to, and elution from, Dynabeads Oligo (dT)25 (Dynal Corp) using the manufacturer's recommended procedures. A random primed cDNA library was prepared using the Superscript Plasmid System (Gibco BRL, Gaithersburg, Md). The random cDNA primer containing an internal Not I restriction site was used to initiate first strand synthesis and had the following sequence:

5'-AAAGGAAGGAAAAAGCGGCCGCTACANNNNNNNNT-3'

(SEQ ID NO:1)

Not I

For the first strand synthesis three separate reactions were assembled that contained 2.5  $\mu$ g of poly(A) RNA and 120 ng, 360 ng or 1,080 ng of random primer. After second strand synthesis, the reaction products were separately extracted with a mixture of phenol:chloroform:isoamyl alcohol (25:24:1 ratio), and then ethanol precipitated. The double strand (ds) cDNA products of the three reactions were combined and ligated to the following ds oligonucleotide adapter:



5'-TCGACCCACGCGTCCG-3' (SEQ ID NO:2)

3'-GGGTGCGCAGGCp-5' (SEQ ID NO:3)

After ligation the cDNA was digested to completion with Not I, extracted with phenol:chloroform:isoamyl (25:24:1) alcohol and ethanol precipitated. The resuspended cDNA was then size fractionated by gel filtration using premade columns provided with the Superscript Plasmid System (Gibco BRL, Gaithersburg, Md) as recommended by the manufacturer. The two fractions containing the largest cDNA products were pooled, ethanol precipitated and then directionally ligated into Not I and Sal I digested pMOB vector DNA (Strathmann *et al*, 1991). The ligated cDNA was introduced into competent ElectromAX DH10B E. coli (Gibco BRL, Gaithersburg, MD) by electroporation. For automated sequence analysis approximately 10,000 transformants were plated on 20cm x 20cm agar plates containing ampicillin supplemented LB nutrient media. The colonies that arose were picked and arrayed onto 96 well microtiter plates containing 200 µl of L-broth, 7.5% glycerol, and 50 µg/ml ampicillin. The cultures were grown overnight at 37°C, a duplicate set of microtiter plates were made using a sterile 96 pin replicating tool, then both sets were stored at -80°C for further analysis. For full-length cDNA cloning approximately one million transformants were plated on 96 bacterial ampicillin plates containing about 10,000 clones each. The plasmid DNA from each pool was separately isolated using the Qiagen Plasmid Maxi Kit (Qiagen Corp., Germany) and arrayed into 96 microtiter plates for PCR analyses.

To sequence random fetal rat intestine cDNA clones, glycerol stocks were thawed, and small aliquots diluted 1:25 in distilled. Approximately 3.0 µl of diluted bacterial cultures were added to PCR reaction



mixture (Boehringer-Mannheim) containing the following oligonucleotides:

5'-TGTAACGACGGCCAGT-3' (SEQ ID NO:4)

5'-CAGGAAACAGCTATGACC-3' (SEQ ID NO:5)

5 The reactions were incubated in a thermocycler (Perkin-Elmer 9600) with the following cycle conditions: 94 C for 2 minutes; 30 cycles of 94°C for 5 seconds, 50°C for 5 seconds, and 72°C for 3 minutes.; 72°C for 4 minutes. After incubation in the  
10 thermocycler, the reactions were diluted with 2.0 mL of water. The amplified DNA fragments were further purified using Centricon columns (Princeton Separations) using the manufacturer's recommended procedures. The PCR reaction products were sequenced on  
15 an Applied Biosystems 373A automated DNA sequencer using T3 primer (oligonucleotide 353-23; 5'-CAATTAACCCTCACTAAAGG-3') (SEQ ID NO:6) Taq dye-terminator reactions (Applied Biosystems) following the manufacturer's recommended procedures.

20 The resulting 5' nucleotide sequence obtained from randomly picked cDNA clones translated and then compared to the existing database of known protein sequences using a modified version of the FASTA program (Pearson et al. Meth. Enzymol. 183, (1990)).  
25 Translated sequences were also analysed for the presence of a specific cysteine-rich protein motif found in all known members of the tumor necrosis factor receptor (TNFR) superfamily (Smith et al. (1994) Cell 76: 959-62), using the sequence profile  
30 method of Gribskov et al. (1987), Proc. Natl. Acad. Sci. USA 83: 4355-9), as modified by Luethy et al. (1994), Protein Science 3: 139-46.

Using the FASTA and Profile search data, an EST, FRI-1 (Fetal Rat Intestine-1), was identified as a  
35 possible new member of the TNFR superfamily. FRI-1



contained an approximately 600 bp insert with a LORF of about 150 amino acids. The closest match in the database was the human type II TNFR (TNFR-II). The region compared showed an about 43% homology between  
5 TNFR-II and FRI-1 over this 150 aa LORF. Profile analysis using the first and second cysteine-rich repeats of the TNFR superfamily yielded a Z score of about 8, indicating that the FRI-1 gene possibly encodes a new family member.

10 To deduce the structure of the FRI-1 product, the fetal rat intestine cDNA library was screened for full length clones. The following oligonucleotides were derived from the original FRI-1 sequence:

5'-GCATTATGACCCAGAAACCGGAC-3' (SEQ ID NO:7)

15 5'-AGGTAGCGCCCTTCCTCACATTC-3' (SEQ ID NO:8)

These primers were used in PCR reactions to screen 96 pools of plasmid DNA, each pool containing plasmid DNA from 10,000 independent cDNA clones. Approximately 1 ug of plasmid pool DNA was amplified in a PCR  
20 reaction mixture (Boehringer-Mannheim) using a Perkin-Elmer 96 well thermal cycler with the following cycle conditions: 2 min at 94°C, 1 cycle; 15 sec at 94°C, then 45 sec at 65°C, 30 cycles; 7 min at 65°C, 1 cycle. PCR reaction products were analysed by gel electrophoresis.  
25 13 out of 96 plasmid DNA pools gave rise to amplified DNA products with the expected relative molecular mass.

DNA from one positive pool was used to transform competent ElectromAX DH10B *E. coli* (Gibco BRL, Gaithersburg, MD) as described above. Approximately  
30 40,000 transformants were plated onto sterile nitrocellulose filters (BA-85, Schleicher and Schuell), and then screened by colony hybridization using a <sup>32</sup>P-dCTP labeled version of the PCR product obtained above. Filters were prehybridized in 5X SSC, 50% deionized  
35 formamide, 5X Denhardt's solution, 0.5% SDS, and 100 ug/ml denatured salmon sperm DNA for 2-4 hours at 42°C.



Filters were then hybridized in 5X SSC, 50% deionized formamide, 2X Denhardt's solution, 0.1% SDS, 100 µg/ml denatured salmon sperm DNA, and about 5 ng/ml of labelled probe for about 18 hours at 42°C. The filters  
5 were then washed in 2X SSC for 10 min at RT, 1X SSC for 10 minutes at 55°C, and finally in 0.5X SSC for 10-15 min at 55°C. Hybridizing clones were detected following autoradiography, and then replated onto nitrocellulose filters for secondary screening. Upon secondary  
10 screening, a plasmid clone (pB1.1) was isolated, then amplified in L-broth media containing 100 ug/ml ampicillin and the plasmid DNA obtained. Both strands of the 2.4 kb pB1.1 insert were sequenced.

The pB1.1 insert sequence was used for a FASTA  
15 search of the public database to detect any existing sequence matches and/or similarities. No matches to any known genes or EST's were found, although there was an approximate 45% similarity to the human and mouse TNFR-II genes. A methionine start codon is found at bp 124  
20 of the nucleotide sequence, followed by a LORF encoding 401 aa residues that terminates at bp 1327. The 401 aa residue product is predicted to have a hydrophobic signal peptide of approximately 31 residues at its N-terminus, and 4 potential sites of N-linked  
25 glycosylation. No hydrophobic transmembrane spanning sequence was identified using the PepPlot program (Wisconsin GCG package, version 8.1). The deduced 401 aa sequence was then used to search the protein database. Again, there were no existing matches,  
30 although there appeared to be a strong similarity to many members of the TNFR superfamily, most notably the human and mouse TNFR-II. A sequence alignment of this novel protein with known members of the TNFR-superfamily was prepared using the Pileup program, and  
35 then modified by PrettyPlot (Wisconsin GCG package,



version 8.1). This alignment shows a clear homology between the full length FRI-1 gene product and all other TNFR family members. The homologous region maps to the extracellular domain of TNFR family members, and corresponds to the three or four cysteine-rich repeats found in the ligand binding domain of these proteins. This suggested that the FRI-1 gene encoded a novel TNFR family member. Since no transmembrane spanning region was detected we predicted that this may be a secreted receptor, similar to TNFR-I derived soluble receptors (Kohno *et al.* (1990), *Proc. Natl. Acad. Sci. USA* 87: 8331-5). Due to the apparent biological activity of the FRI-1 gene (*vide infra*), the product was named Osteoprotegerin (OPG).

15

#### EXAMPLE 2

##### OPG mRNA Expression Patterns in Tissues

Multiple human tissue northern blots (Clontech) were probed with a <sup>32</sup>P-dCTP labelled FRI-1 PCR product to detect the size of the human transcript and to determine patterns of expression. Northern blots were prehybridized in 5X SSPE, 50% formamide, 5X Denhardt's solution, 0.5% SDS, and 100 µg/ml denatured salmon sperm DNA for 2-4 hr at 42°C. The blots were then hybridized in 5X SSPE, 50% formamide, 2X Denhardt's solution, 0.1% SDS, 100 µg/ml denatured salmon sperm DNA, and 5 ng/ml labelled probe for 18-24 hr at 42°C. The blots were then washed in 2X SSC for 10 min at room temperature, 1X SSC for 10 min at 50°C, then in 0.5X SSC for 10-15 min.

30

Using a probe derived from the rat gene, a predominant mRNA species with a relative molecular mass of about 2.4 kb is detected in several tissues, including kidney, liver, placenta, and heart. Highest levels are detected in the kidney. A large mRNA species of Mr 4.5 and 7.5 kb was detected in skeletal muscle

35



and pancreas. In human fetal tissue, kidney was found to express relatively high levels of the 2.4 kb mRNA. Using a human probe (vide infra), only the 2.4 kb transcript is detected in these same tissues. In addition, relatively high levels of the 2.4 kb transcript was detected in the lymph node, thymus, spleen and appendix. The size of the transcript detected by both the rat and human Osteosprotegerin gene is almost identical to the length of the rat pBl.1 FRI-1 insert, suggesting it was a full length cDNA clone.

### EXAMPLE 3

#### Systemic delivery of OPG in transgenic mice

The rat OPG clone pBl.1 was used as template to PCR amplify the coding region for subcloning into an ApoE-liver specific expression vector (Simonet *et al.* J. Clin. Invest. 94, 1310-1319 (1994), and PCT Application No. US94/11675 and co-owned U.S. Serial No. 08/221,767. The following 5' and 3' oligonucleotide primers were used for PCR amplification, respectively:

5'-GACTAGTCCCACAATGAACAAGTGGCTGTG-3'

(SEQ ID NO:9)

5'-ATAAGAATGCGGCCGCTAAACTATGAAACAGCCCAGTGACCATTC-3'

(SEQ ID NO:10)

The PCR reaction mixture (Boehringer-Mannheim) was treated as follows: 94°C for 1 minute, 1 cycle; 94°C for 20 sec, 62°C for 30 sec, and 74 C for 1 minute, 25 cycles. Following amplification, the samples were purified over Qiagen PCR columns and digested overnight with SpeI and NotI restriction enzymes. The digested products were extracted and precipitated and subcloned into the ApoE promoter expression vector. Prior to microinjecting the resulting clone, HE-OPG, it was sequenced to ensure it was mutation-free.

The HE-OPG plasmid was purified through two rounds of CsCl density gradient centrifugation. The purified



plasmid DNA was digested with XhoI and Ase I, and the 3.6 kb transgene insert was purified by gel electrophoresis. The purified fragment was diluted to a stock injection solution of 1 µg/ml in 5 mM Tris, pH 7.4, 0.2 mM EDTA. Single-cell embryos from BDF1 x BDF1-bred mice were injected essentially as described (Brinster *et al.* (1985), *Proc. Natl. Acad. Sci. USA* 82: 4338), except that injection needles were beveled and siliconized before use. Embryos were cultured overnight in a CO<sub>2</sub> incubator and 15 to 20 2-cell embryos were transferred to the oviducts of pseudopregnant CD1 female mice.

Following term pregnancy, 49 offspring were obtained from implantation of microinjected embryos. The offspring were screened by PCR amplification of the integrated transgene in genomic DNA samples. The target region for amplification was a 369 bp region of the human Apo E intron which was included in the expression vector. The oligos used for PCR amplification were:

5'- GCC TCT AGA AAG AGC TGG GAC-3' (SEQ ID NO:11)  
5'- CGC CGT GTT CCA TTT ATG AGC-3' (SEQ ID NO:12)

The conditions for PCR were: 94°C for 2 minute, 1 cycle; 94°C for 1 min, 63°C for 20 sec, and 72°C for 30 sec, 30 cycles. Of the 49 original offspring, 9 were identified as PCR positive transgenic founders.

At 8-10 weeks of age, five transgenic founders (2, 11, 16, 17, and 28) and five controls (1, 12, 15, 18, and 30) were sacrificed for necropsy and pathological analysis. Liver was isolated from the remaining 4 founders by partial hepatectomy. For partial hepatectomy, the mice were anesthetized and a lobe of liver was surgically removed. Total cellular RNA was isolated from livers of all transgenic founders, and 5 negative control littermates as described (McDonald *et al.* *Meth. Enzymol.* 152, 219 (1987)). Northern blot



analysis was performed on these samples to assess the level of transgene expression. Approximately 10ug of total RNA from each animal liver was resolved by electrophoresis denaturing gels (Ogden *et al.* Meth. Enzymol 152, 61 (1987)), then transferred to HYBOND-N nylon membrane (Amersham), and probed with <sup>32</sup>P dCTP-labelled pB1.1 insert DNA. Hybridization was performed overnight at 42°C in 50% Formamide, 5 x SSPE, 0.5% SDS, 5 x Denhardt's solution, 100 µg/ml denatured salmon sperm DNA and 2-4 x 10<sup>6</sup> cpm of labeled probe/ml of hybridization buffer. Following hybridization, blots were washed twice in 2 x SSC, 0.1% SDS at room temperature for 5 min each, and then twice in 0.1 x SSC, 0.1% SDS at 55°C for 5-10 min each. Expression of the transgene in founder and control littermates was determined following autoradiography.

The northern blot data indicate that 7 of the transgenic founders express detectable levels of the transgene mRNA (animal #'s 2,11,16,17,22,33,and 45). The negative control mice and one of the founders (#28) expressed no transgene-related mRNA. Since OPG is predicted to be a secreted protein, overexpression of transgene mRNA should be a proxy for the level of systemically delivered gene product. Of the PCR and northern blot positive mice, animal 2, 17 and 22 expressed the highest levels of transgene mRNA, and may show more extensive biological effects on host cells and tissues.

#### EXAMPLE 4

##### Biological activity of OPG

Five of the transgenic mice (animals 2,11,16,17 and 28) and 5 control littermates (animals 1,12,15,18, and 30) were sacrificed for necropsy and pathological analysis using the following procedures:



Prior to euthanasia, all animals had their identification numbers verified, then were weighed, anesthetized and blood drawn. The blood was saved as both serum and whole blood for a complete serum chemistry and hematology panel. Radiography was performed just after terminal anesthesia by lethal CO<sub>2</sub> inhalation, and prior to the gross dissection. Following this, tissues were removed and fixed in 10% buffered Zn-Formalin for histological examination. The tissues collected included the liver, spleen, pancreas, stomach, duodenum, ileum, colon, kidney, reproductive organs, skin and mammary glands, bone, brain, heart, lung, thymus, trachea, esophagus, thyroid, jejunum, cecum, rectum, adrenals, urinary bladder, and skeletal muscle. Prior to fixation the whole organ weights were determined for the liver, stomach, kidney, adrenals, spleen, and thymus. After fixation the tissues were processed into paraffin blocks, and 3  $\mu$ m sections were obtained. Bone tissue was decalcified using a formic acid solution, and all sections were stained with hematoxylin and eosin. In addition, staining with Gomori's reticulin and Masson's trichrome were performed on certain tissues. Enzyme histochemistry was performed to determine the expression of tartrate resistant acid phosphatase (TRAP), an enzyme highly expressed by osteoclasts, multinucleated bone-resorbing cells of monocyte-macrophage lineage. Immunohistochemistry for BrdU and F480 monocyte-macrophage surface antigen was also performed to detect replicating cells and cells of the monocyte-macrophage lineage, respectively. To detect F480 surface antigen expression, formalin fixed, paraffin embedded 4  $\mu$ m sections were deparaffinized and hydrated to deionized water. The sections were quenched with 3% hydrogen peroxide, blocked with Protein Block (Lipshaw, Pittsburgh, PA), and incubated in rat monoclonal anti-



mouse F480 (Harlan, Indianapolis, IN). This antibody was detected by biotinylated rabbit anti-rat immunoglobulins, peroxidase conjugated streptavidin (BioGenex San Ramon, CA) with DAB as chromagen (BioTek, Santa Barbara, CA). Sections were counterstained with hematoxylin.

Upon gross dissection and observation of visceral tissues, no abnormalities were found in the transgene expressors or control littermates. Analysis of organ weight indicate that spleen size increased by approximately 38% in the transgenic mice relative to controls. There was a slight enlargement of platelet size and increased circulating unstained cells in the transgene expressors. There was a marginal decrease in platelet levels in the transgene expressors. In addition, the serum uric acid, urea nitrogen, and alkaline phosphatase levels all trended lower in the transgene expressors. The expressors were found to have increased radiodensity of the skeleton, including long bones (femurs), vertebrae, and flat bones (pelvis). The relative size of femurs in the expressors were not different from the the control mice.

Histological analysis of stained sections of bone from the OPG expressors show severe osteopetrosis with the presence of cartilage remnants from the primary spongiosa seen within bone trabeculae in the diaphysis of the femur. A clearly defined cortex was not identifiable in the sections of femur. In normal animals, the central diaphysis is filled with bone marrow. Sections of vertebra also show osteopetrotic changes implying that the OPG-induced skeletal changes were systemic. The residual bone marrow showed predominantly myeloid elements. Megakaryocytes were present. Reticulin stains showed no evidence for reticulin deposition. Immunohistochemistry for F480, a cell surface antigen expressed by cells of monocyte-



macrophage derivation in the mouse, showed the presence of F480 positive cells in the marrow spaces. Focally, flattened F480 positive cells could be seen directly adjacent to trabecular bone surfaces.

5       The mesenchymal cells lining the bony trabeculae were flattened and appeared inactive. Based on H&E and TRAP stains, osteoclasts were rarely found on the trabecular bone surfaces in the OPG expressors. In contrast, osteoclasts and/or chondroclasts were seen in  
10 the region of the growth plate resorbing cartilage, but their numbers may be reduced compared to controls. Also, osteoclasts were present on the cortical surface of the metaphysis where modelling activity is usually robust. The predominant difference between the  
15 expressors and controls was the profound decrease in trabecular osteoclasts, both in the vertebrae and femurs. The extent of bone accumulation was directly correlated with the level of OPG transgene mRNA detected by northern blotting of total liver RNA.

20       The spleens from the OPG expressors had an increased amount of red pulp with the expansion due to increased hematopoiesis. All hematopoietic lineages are represented. F480 positive cells were present in both control and OPG expressors in the red pulp. Two of the  
25 expressors (2 and 17) had foci of extramedullary hematopoiesis within the liver and this is likely due to the osteopetrotic marrow.

There were no observable abnormalities in the thymus, lymph nodes, gastrointestinal tract, pancreato-  
30 hepatobiliary tract, respiratory tract, reproductive system, genito-urinary system, skin, nervous system, heart and aorta, breast, skeletal muscle and fat.

#### EXAMPLE 5

##### Isolation of mouse and human OPG cDNA

35       A cDNA clone corresponding to the 5' end of the mouse OPG mRNA was isolated from a mouse kidney cDNA



library (Clontech) by PCR amplification. The oligonucleotides were derived from the rat OPG cDNA sequence and are shown below:

5'-ATCAAAGGCAGGGCATACTTCCTG-3' (SEQ ID NO:13)  
5'-GTTGCACTCCTGTTTCACGGTCTG-3' (SEQ ID NO:14)  
5'-CAAGACACCTTGAAGGGCCTGATG-3' (SEQ ID NO:15)  
5'-TAACTTTTACAGAAGAGCATCAGC-3' (SEQ ID NO:16)

5'-AGCGCGGCCCGCATGAACAAGTGGCTGTGCTGCG-3' (SEQ ID NO:17)  
5'-AGTCTAGAGAAACAGCCAGTGACCATTCC-3' (SEQ ID NO:18)

The partial and full-length cDNA products obtained in this process were sequenced. The full-length product was digested with Not I and XbaI, then directionally cloned into the plasmid vector pRcCMV (Invitrogen). The resulting plasmid was named pRcCMV-Mu-OPG. The nucleotide sequence of the cloned product was compared to the rat OPG cDNA sequence. Over the 1300 bp region spanning the OPG LORF, the rat and mouse DNA sequences are approximately 88% identical. The mouse cDNA sequence contained a 401 aa LORF, which was compared to the rat OPG sequence and found to be about 94% identical without gaps. This indicates that the mouse cDNA sequence isolated encodes the murine OPG, and that the sequence and structure has been highly conserved throughout evolution. The mouse OPG sequence contains an identical putative signal peptide at its N-terminus, and all 4 potential sites of N-linked glycosylation are conserved.

A partial human OPG cDNA was cloned from a human kidney cDNA library using the following rat-specific oligonucleotides:

5'-GTG AAG CTG TGC AAG AAC CTG ATG-3' (SEQ ID NO:19)  
5'-ATC AAA GGC AGG GCA TAC TTC CTG-3' (SEQ ID NO:20)

This PCR product was sequenced and used to design primers for amplifying the 3' end of the human cDNA using a human OPG genomic clone in lambda as template:

5'-TCCGTAAGAAACAGCCAGTGACC-3' (SEQ ID NO:29)



5'-CAGATCCTGAAGCTGCTCAGTTG-3' (SEQ ID NO:21)

The amplified PCR product was sequenced, and together with the 5' end sequence, was used to design 5' and 3' human-specific primers useful for amplifying the entire human OPG cDNA coding sequences:

5'-AGCGCGGCCGCGGGGACCACAATGAACAAGTTG-3' (SEQ ID NO:22)

5'-AGCTCTAGAATTGTGAGGAAACAGCTCAATGGC-3' (SEQ ID NO:23)

The full-length human PCR product was sequenced, then directionally cloned into the plasmid vector pRcCMV (Invitrogen) using Not I and Xba I. The resulting plasmid was named pRcCMV-human OPG. The nucleotide sequence of the cloned product was compared to the rat and mouse OPG cDNA sequences. Over the 1300 bp region spanning the OPG LORF, the rat and mouse DNA sequences are approximately 78-88% identical to the human OPG cDNA. The human OPG cDNA sequence also contained a 401 aa LORF, and it was compared to the rat and mouse protein sequences. The predicted human OPG is approximately 85% identical, and about 90% identical to the rat and mouse proteins, respectively. Sequence alignment of rat, mouse and human proteins show that they have been highly conserved during evolution. The human protein is predicted to have a N-terminal signal peptide, and 5 potential sites of N-linked glycosylation, 4 of which are conserved between the rat and mouse OPG.

The DNA and predicted amino acid sequence of mouse OPG is shown in Figure 9A and 9B (SEQ ID NO:122). The DNA and predicted amino acid sequence of human OPG is shown in Figure 9C and 9D (SEQ ID NO:124). A comparison of the rat, mouse and human OPG amino acid sequences is shown in Figure 9E and 9F.

Isolation of additional human OPG cDNA clones revealed the presence of a G to C base change at position 103 of the DNA sequence shown in Figure 9C. This nucleotide change results in substitution of an



asparagine for a lysine at position 3 of the amino acid sequence shown in Figure 9C. The remainder of the sequence in clones having this change was identical to that in Figure 9C and 9D.

5

#### EXAMPLE 6

##### OPG three-dimensional structure modelling

The amino-terminal portion of OPG has homology to the extracellular portion of all known members of the TNFR superfamily (Figure 1C). The most notable motif in  
10 this region of TNFR-related genes is an about 40 amino acid, cysteine-rich repeat sequence which folds into distinct structures (Banner et al. (1993), Cell 73: 431-45). This motif is usually displayed in four (range 3-6) tandem repeats (see Figure 1C), and is known to be  
15 involved in ligand binding (Beutler and van Huffel (1994), Science 264: 667-73). Each repeat usually contains six interspaced cysteine residues, which are involved in forming three intradomain disulfide bonds, termed SS1, SS2, and SS3 (Banner et al., ibid). In some  
20 receptors, such as TNFR2, CD30 and CD40, some of the repeat domains contain only two intrachain disulfide bonds (SS1 and SS3).

The human OPG sequence was aligned to a TNFR1 extracellular domain profile using methods described by  
25 Luethy, et al., ibid, and the results were graphically displayed using the PrettyPlot program from the Wisconsin Package, version 8.1 (Genetics Computer Group, Madison, WI) (Figure 10). The alignment indicates a clear conservation of cysteine residues  
30 involved in formation of domains 1-4. This alignment was then used to construct a three-dimensional (3-D) model of the human OPG N-terminal domain using the known 3-D structure of the extracellular domain of p55 TNFR1 (Banner et al., ibid) as the template. To do this  
35 the atomic coordinates of the peptide backbone and side chains of identical residues were copied from the



crystal structure coordinates of TNFR1. Following this, the remaining coordinates for the insertions and different side chains were generated using the LOOK program (Molecular Applications Group, Palo Alto, CA).

- 5 The 3-D model was then refined by minimizing its conformational energy using LOOK.

By analogy with other TNFR family members, it is assumed that OPG binds to a ligand. For the purpose of modelling the interaction of OPG with its ligand, the crystal structure of TNF- $\beta$  was used to simulate a 3-D representation of an "OPG ligand". This data was graphically displayed (see Figure 11) using Molscript (Kraulis (1991), J. Appl. Cryst. 24: 946-50). A model for the OPG/ligand complex with 3 TNF $\beta$  and 3 OPG molecules was constructed where the relative positions of OPG are identical to TNFR1 in the crystal structure. This model was then used to find the residues of OPG that could interact with its ligand using the following approach: The solvent accessible area of all residues in the complex and one single OPG model were calculated. The residues that have different accessibility in the complex than in the monomer are likely to interact with the ligand.

The human and mouse OPG amino acid sequences were realigned using this information to highlight sequences comprising each of the cysteine rich domains 1-4 (Figure 12A and 12B). Each domain has individual structural characteristics which can be predicted.

Domain 1: Contains 4 cysteines involved in SS2 (C41 to C54) and SS3 (C44 to C62) disulfide bonds. Although no SS1 bond is evident based on disulfide bridges, the conserved tyrosine at position 28 is homologous to Y20 in TNFR1, which is known to be involved in interacting with H66 to aid in domain formation. OPG has a homologous histidine at position



75, suggesting OPG Y28 and H75 stack together in the native protein, as do the homologous residues in TNFR1. Therefore, both of these residues may indeed be important for biological activity, and N-terminal OPG truncations up to and beyond Y28 may have altered activity. In addition, residues E34 and K43 are predicted to interact with a bound ligand based on our 3-dimensional model.

Domain 2: Contains six cysteines and is predicted to contain SS1 (C65 to C80), SS2 (C83 to C98) and SS3 (C87 to C105) disulfide bonds. This region of OPG also contains an region stretching from P66-Q91 which aligns to the portion of TNFR1 domain 2 which forms close contacts with TNF $\beta$  (see above), and may interact with an OPG ligand. In particular residues P66, H68, Y69, Y70, T71, D72, S73, H75, T76, S77, D78, E79, L81, Y82, P85, V86, K88, E89, L90, and Q91 are predicted to interact with a bound ligand based on our structural data.

Domain 3: Contains 4 cysteines involved in SS1 (C107 to C 118) and SS3 (C124 to C142) disulfide bonds, but not an SS2 bond. Based on our structural data, residues E115, L118 and K119 are predicted in to interact with an OPG ligand.

Domain 4: Contains 4 cysteines involved in SS1 (C145 to C160) and SS3 (C166 to C185) disulfide bonds, but not an SS2 bond, similar to domain 3. Our structural data predict that E153 and S155 interact with an OPG ligand.

Thus, the predicted structural model for OPG identifies a number of highly conserved residues which are likely to be important for its biological activity.

#### EXAMPLE 7

#### Production of recombinant secreted OPG in mammalian cells



To determine if OPG is actually a secreted protein, mouse OPG cDNA was fused to the human IgG1 Fc domain as a tag (Capon *et al.* Nature 337, 525-531 (1989)), and expressed in human 293 fibroblasts. Fc fusions were carried out using the vector pFc-A3. pFc-A3 contains the region encoding the Fc portion of human immunoglobulin IgG- $\gamma$ 1 heavy chain (Ellison *et al.* *ibid*) from the first amino acid of the hinge domain (Glu-99) to the carboxyl terminus and is flanked by a 5'-NotI fusion site and 3'-SalI and XbaI sites. The plasmid was constructed by PCR amplification of the human spleen cDNA library (Clontech). PCR reactions were in a final volume of 100  $\mu$ l and employed 2 units of Vent DNA polymerase (New England Biolabs) in 20 mM Tris-HCl (pH 8.8), 10 mM KCl, 10  $\mu$ M (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub>, 2 mM MgSO<sub>4</sub>, 0.1% Triton X-100 with 400  $\mu$ M each dNTP and 1 ng of the cDNA library to be amplified together with 1  $\mu$ M of each primer. Reactions were initiated by denaturation at 95°C for 2 min, followed by 30 cycles of 95°C for 30 s, 55°C for 30 s, and 73°C for 2 min. The 5' primer

5' ATAGCGGCCGCTGAGCCCAATCTTGTGACAAACTCAC 3'  
(SEQ ID NO:24)

incorporated a NotI site immediately 5' to the first residue (Glu-99) of the hinge domain of IgG- $\gamma$ 1. The 3' primer

5'-TCTAGAGTCGACTTATCATTTACCCGGAGACAGGGAGAGGCTCTT-3'  
(SEQ ID NO:25)

incorporated SalI and XbaI sites. The 717-bp PCR product was digested with NotI and SalI, isolated by electrophoresis through 1% agarose (FMC Corp.), purified by the GeneClean procedure (BIO 101, Inc.) and cloned into NotI, SalI-digested pBluescript II KS vector (Stratagene). The insert in the resulting plasmid, pFc-A3, was sequenced to confirm the fidelity of the PCR reaction.



The cloned mouse cDNA in plasmid pRcCMV-MuOPG was amplified using the following two sets of primer pairs:

Pair 1:

5'-CCTCTGAGCTCAAGCTTCCGAGGACCACAATGAACAAG-3'

5 (SEQ ID NO:26)

5'-CCTCTGCGGCCGCTAAGCAGCTTATTTTCACGGATTGAACCTG-3'

(SEQ ID NO:27)

Pair 2:

5'-CCTCTGAGCTCAAGCTTCCGAGGACCACAATGAACAAG-3'

10 (SEQ ID NO:28)

5'-CCTCTGCGGCCGCTGTTGCATTTCTTCTG-3'

(SEQ ID NO:30)

The first pair amplifies the entire OPG LORF, and creates a NotI restriction site which is compatible with the in-frame Not I site in Fc fusion vector pFcA3. pFcA3 was prepared by engineering a NotI restriction site 5' to aspartic acid residue 216 of the human IgG1 Fc cDNA. This construct introduces a linker which encodes two irrelevant amino acids which span the junction between the OPG and IgG Fc region. This product, when linked to the Fc portion, would encode all 401 OPG residues directly followed by all 227 amino acid residues of the human IgG1 Fc region (F1.Fc). The second primer pair amplifies the DNA sequences encoding the first 180 amino acid residues of OPG, which encompasses its putative ligand binding domain. As above, the 3' primer creates an artificial Not I restriction site which fuses the C-terminal truncated OPG LORF at position threonine 180 directly to the IgG1 Fc domain (CT.fc).

The amino acid sequence junction linking OPG residue 401 and aspartic acid residue 221 of the human Fc region can be modified as follows: The DNA encoding residues 216-220 of the human Fc region can be deleted as described below, or the cysteine residue corresponding to C220 of the human Fc region can be



mutated to either serine or alanine. OPF-Fc fusion protein encoded by these modified vectors can be transfected into human 293 cells, or CHO cells, and recombinant OPG-Fc fusion protein purified as described  
5 below.

Both products were directionally cloned into the plasmid vector pCEP4 (Invitrogen). pCEP4 contains the Epstein-Barr virus origin of replication, and is capable of episomal replication in 293-EBNA-1 cells.  
10 The parent pCEP4, and pCEP4-F1.Fc and pCEP4-CT.Fc vectors were lipofected into 293-EBNA-1 cells using the manufacturer's recommended methods. The transfected cells were then selected in 100 µg/ml hygromycin to select for vector expression, and the resulting drug-  
15 resistant mass cultures were grown to confluence. The cells were then cultured in serum-free media for 72 hr, and the conditioned media removed and analysed by SDS-PAGE. A silver staining of the polyacrylamide gel detects the major conditioned media proteins produced  
20 by the drug resistant 293 cultures. In the pCEP4-F1.Fc and the pCEP4-CT.Fc conditioned media, unique bands of the predicted sizes were abundantly secreted (see Figures 13B and 13C). The full-length Fc fusion protein accumulated to a high concentration, indicating that it  
25 may be stable. Both Fc fusion proteins were detected by anti-human IgG1 Fc antibodies (Pierce) on western blots, indicating that they are recombinant OPG products.

The full length OPG-Fc fusion protein was purified  
30 by Protein-A column chromatography (Pierce) using the manufacturers recommended procedures. The protein was then subjected to N-terminal sequence analysis by automated Edman degradation as essentially described by Matsudaira et al. (J. Biol. Chem. 262, 10-35 (1987)).



The following amino acid sequence was read after 19 cycles:

NH<sub>2</sub>-E T L P P K Y L H Y D P E T G H Q L L-CO<sub>2</sub>H  
(SEQ ID NO:31)

- 5 This sequence was identical to the predicted mouse OPG amino acid sequence beginning at amino acid residue 22, suggesting that the natural mammalian leader cleavage site is between amino acid residues Q21-E22, not between Y31-D32 as originally predicted. The  
10 expression experiments performed in 293-EBNA cells with pCEP4-F1.Fc and pCEP4-CT.Fc demonstrate that OPG is a secreted protein, and may act systemically to bind its ligand.

- Procedures similar to those used to construct and  
15 express the muOPG[22-180]-Fc and muOPG[22-401]-Fc fusions were employed for additional mouse and human OPG-Fc fusion proteins.

- Murine OPG cDNA encoding amino acids 1-185 fused to the Fc region of human IgG1 [muOPG Ct(185).Fc] was  
20 constructed as follows. Murine OPG cDNA from plasmid pRCCMV Mu Osteoprotegerin (described in Example 5) was amplified using the following primer pair in a polymerase chain reaction as described above:

1333-82:

- 25 5'-TCC CTT GCC CTG ACC ACT CTT-3'  
(SEQ ID NO:32)

1333-80:

5'-CCT CTG CCG CCG CAC ACA CGT TGT CAT GTG TTG C-3'  
(SEQ ID NO:33)

- 30 This primer pair amplifies the murine OPG cDNA region encoding amino acid residues 63-185 (corresponding to bp 278-645) of the OPG reading frame as shown in Figure 9A. The 3' primer contains a Not I restriction site which is compatible with the in-frame  
35 Not I site of the Fc fusion vector pFcA3. The product also spans a unique EcoRI restriction site located at



bp 436. The amplified PCR product was purified, cleaved with NotI and EcoRI, and the resulting EcoRI-NotI restriction fragment was purified. The vector pCEP4 having the murine 1-401 OPG-Fc fusion insert was  
5 cleaved with EcoRI and NotI, purified, and ligated to the PCR product generated above. The resulting pCEP4-based expression vector encodes OPG residues 1-185 directly followed by all 227 amino acid residues of the human IgG1 Fc region. The murine OPG 1-185.Fc fusion  
10 vector was transfected into 293 cells, drug selected, and conditioned media was produced as described above. The resulting secreted murine OPG 1-185.Fc fusion product was purified by Protein-A column chromatography (Pierce) using the manufacturers recommended  
15 procedures.

Murine OPG DNA encoding amino acid residues 1-194 fused to the Fc region of human IgG1 (muOPG Ct(194).Fc) was constructed as follows. Mouse OPG cDNA from plasmid pRCCMV Mu-Osteoprotegerin was amplified using the  
20 following primer pairs:

1333-82:

5'-TCC CTT GCC CTG ACC ACT CTT-3'  
(SEQ ID NO:34)

1333-81:

25 5'-CCT CTG CGG CCG CCT TTT GCG TGG CTT CTC TGT T-3'  
(SEQ ID NO:35)

This primer pair amplifies the murine OPG cDNA region encoding amino acid residues 70-194 (corresponding to bp 298-672) of the OPG reading frame.  
30 The 3' primer contains a Not I restriction site which is compatible with the in-frame Not I site of the Fc fusion vector pFcA3. The product also spans a unique EcoRI restriction site located at bp 436. The amplified PCR product was cloned into the murine OPG[1-401] Fc  
35 fusion vector as described above. The resulting pCEP4-based expression vector encodes OPG residues 1-194



directly followed by all 227 amino acid residues of the human IgG1 Fc region. The murine OPG 1-194.Fc fusion vector was transfected into 293 cells, drug selected, and conditioned media was produced. The resulting  
5 secreted fusion product was purified by Protein-A column chromatography (Pierce) using the manufacturers recommended procedures.

Human OPG DNA encoding amino acids 1-401 fused to the Fc region of human IgG1 was constructed as follows.  
10 Human OPG DNA in plasmid pRcCMV-hu osteoprotegerin (described in Example 5) was amplified using the following oligonucleotide primers:

1254-90:

5'-CCT CTG AGC TCA AGC TTG GTT TCC GGG GAC CAC AAT G-3'

15 (SEQ ID NO:36)

1254-95:

5'-CCT CTG CGG CCG CTA AGC AGC TTA TTT TTA CTG AAT GG-3'

(SEQ ID NO:37)

The resulting PCR product encodes the full-length  
20 human OPG and creates a Not I restriction site which is compatible with the in-frame Not I site Fc fusion vector Fca3. The PCR product was directionally cloned into the plasmid vector pCEP4 as described above. The resulting expression vector encodes human OPG residues  
25 1-401 directly followed by 227 amino acid residues of the human IgG1 Fc region. Conditioned media from transfected and drug selected cells was produced and the huOPG F1.Fc fusion product was purified by Protein-A column chromatography (Pierce) using the  
30 manufacturers recommended procedures.

Human OPG DNA encoding amino acid residues 1-201 fused to the Fc region of human IgG1 [huOPG Ct(201).Fc] was constructed as follows. The cloned human OPG cDNA from plasmid pRrCMV-hu osteoprotegerin was amplified by  
35 PCR using the following oligonucleotide primer pair:

1254-90:



5'-CCT CTG AGC TCA AGC TTG GTT TCC GGG GAC CAC AAT G-3'  
(SEQ ID NO:38)

1254-92:

5'-CCT CTG CGG CCG CCA GGG TAA CAT CTA TTC CAC-3'

5 (SEQ ID NO:39)

This primer pair amplifies the human OPG cDNA region encoding amino acid residues 1-201 of the OPG reading frame, and creates a Not I restriction site at the 3' end which is compatible with the in-frame Not I site Fc fusion vector FcA3. This product, when linked to the Fc portion, encodes OPG residues 1-201 directly followed by all 221 amino acid residues of the human IgG1 Fc region. The PCR product was directionally cloned into the plasmid vector pCEP4 as described above. Conditioned media from transfected and drug selected cells was produced, and the hu OPG Ct(201).Fc fusion products purified by Protein-A column chromatography (Pierce) using the manufacturer's recommended procedures.

20 The following procedures were used to construct and express unfused mouse and human OPG.

A plasmid for mammalian expression of full-length murine OPG (residues 1-401) was generated by PCR amplification of the murine OPG cDNA insert from pRcCMV Mu-Osteoprotegerin and subcloned into the expression vector pDSRα (DeClerck et. al. J. Biol. Chem. 266, 3893 (1991)). The following oligonucleotide primers were used:

1295-26:

30 5'-CCG AAG CTT CCA CCA TGA ACA AGT GGC TGT GCT GC-3'  
(SEQ ID NO:40)

1295-27:

5'-CCT CTG TCG ACT ATT ATA AGC AGC TTA TTT TCA CGG ATT G-3'  
(SEQ ID NO:41)

35 The murine OPG full length reading frame was amplified by PCR as described above. The PCR product



was purified and digested with restriction endonucleases Hind III and XbaI (Boehringer Mannheim, Indianapolis, IN) under the manufacturers recommended conditions, then ligated to Hind III and Xba I digested pDSR $\alpha$ . Recombinant clones were detected by restriction endonuclease digestion, then sequenced to ensure no mutations were produced during the PCR amplification steps.

The resulting plasmid, pDSR $\alpha$ -muOPG was introduced into Chinese hamster ovary (CHO) cells by calcium mediated transfection (Wigler et al. (1977), Cell 11: 233). Individual colonies were selected based upon expression of the dihydrofolate reductase (DHFR) gene in the plasmid vector and several clones were isolated. Expression of the murine OPG recombinant protein was monitored by western blot analysis of CHO cell conditioned media. High expressing cells were selected, and OPG expression was further amplified by treatment with methotrexate as described (DeClerck et al., ibid.). Conditioned media from CHO cell lines was produced for further purification of recombinant secreted murine OPG.

A plasmid for mammalian expression of full-length human OPG (amino acids 1-401) was generated by subcloning the cDNA insert in pRcCMV-hu Osteoprotegerin directly into vector pDSR $\alpha$  (DeClerck et al., ibid.). The pRcCMV-OPG plasmid was digested to completion with Not I, blunt ended with Klenow, then digested to completion with XbaI. Vector DNA was digested with HindIII, blunt ended with Klenow, then digested with XbaI, then ligated to the OPG insert. Recombinant plasmids were then sequenced to confirm proper orientation of the human OPG cDNA.

The resulting plasmid pDSR $\alpha$ -huOPG was introduced into Chinese hamster ovary (CHO) cells as described



above. Individual colonies were selected based upon expression of the dihydrofolate reductase (DHFR) gene in the plasmid vector and several clones were isolated. Expression of the human OPG recombinant protein was  
5 monitored by western blot analysis of CHO cell conditioned media. High expressing clones were selected, and OPG expression was further amplified by treatment with methotrexate. Conditioned media from CHO cell lines expressing human OPG was produced for  
10 protein purification.

Expression vectors for murine OPG encoding residues 1-185 were constructed as follows. Murine OPG cDNA from pRCCMV-Mu OPG was amplified using the following oligonucleotide primers:

15 1333-82:

5'-TCC CTT GCC CTG ACC ACT CTT-3' (SEQ ID NO:42)

1356-12:

5'-CCT CTG TCG ACT TAA CAC ACG TTG TCA TGT GTT GC-3'  
(SEQ ID NO:43)

20 This primer pair amplifies the murine OPG cDNA region encoding amino acids 63-185 of the OPG reading frame (bp 278-645) and contains an artificial stop codon directly after the cysteine codon (C185), which is followed by an artificial Sal I restriction  
25 endonuclease site. The predicted product contains an internal Eco RI restriction site useful for subcloning into a pre-existing vector. After PCR amplification, the resulting purified product was cleaved with Eco RI and Sal I restriction endonucleases, and the large  
30 fragment was gel purified. The purified product was then subcloned into the large restriction fragment of an Eco RI and Sal I digest of pBluescript-muOPG Fl.Fc described above. The resulting plasmid was digested with Hind III and Xho I and the small fragment was gel  
35 purified. This fragment, which contains a open reading frame encoding residues 1-185 was then subcloned into a



Hind III and Xho I digest of the expression vector pCEP4. The resulting vector, pmuOPG [1-185], encodes a truncated OPG polypeptide which terminates at a cysteine residue located at position 185. Conditioned media from transfected and drug selected cells was produced as described above.

1333-82:

5'-TCC CTT GCC CTG ACC ACT CTT-3' (SEQ ID NO:44)

1356-13:

10 5'-CCT CTG TCG ACT TAC TTT TGC GTG GCT TCT CTG TT-3'  
(SEQ ID NO:45)

This primer pair amplifies the murine OPG cDNA region encoding amino acids 70-194 of the OPG reading frame (bp 298-672) and contains an artificial stop codon directly after the lysine codon (K194), which is followed by an artificial Sal I restriction endonuclease site. The predicted product contains an internal Eco RI restriction site useful for subcloning into a pre-existing vector. After PCR amplification, the resulting purified product was cleaved with Eco RI and Sal I restriction endonucleases, and the large fragment was gel purified. The purified product was then subcloned into the large restriction fragment of an Eco RI and Sal I digest of pBluescript-muOPG F1.Fc described above. The resulting plasmid was digested with Hind III and Xho I and the small fragment was gel purified. This fragment, which contains a open reading frame encoding residues 1-185 was then subcloned into a Hind III and Xho I digest of the expression vector pCEP4. The resulting vector, pmuOPG [1-185], encodes a truncated OPG polypeptide which terminates at a lysine at position 194. Conditioned media from transfected and drug selected cells was produced as described above.

Several mutations were generated at the 5' end of the huOPG [22-401]-Fc gene that introduce either amino acid substitutions, or deletions, of OPG between



residues 22 through 32. All mutations were generated with the "QuickChange" Site-Directed Mutagenesis Kit" (Stratagene, San Diego, CA) using the manufacturer's recommended conditions. Briefly, reaction mix  
5 containing huOPG [22-401]-Fc plasmid DNA template and mutagenic primers were treated with Pfu polymerase in the presence of deoxynucleotides, then amplified in a thermocycler as described above. An aliquot of the reaction is then transfected into competent *E. coli*  
10 XL1-Blue by heatshock, then plated. Plasmid DNA from transformants was then sequenced to verify mutations.

The following primer pairs were used to delete residues 22-26 of the human OPG gene, resulting in the production of a huOPG [27-401]-Fc fusion protein:

15 1436-11:

5'-TGG ACC ACC CAG AAG TAC CTT CAT TAT GAC-3' (SEQ ID NO:140)

1436-12:

5'-GTC ATA ATG AAG GTA CTT CTG GGT GGT CCA-3' (SEQ ID NO:141)

The following primer pairs were used to delete  
20 residues 22-28 of the human OPG gene, resulting in the production of a huOPG [29-401]-Fc fusion protein:

1436-17:

5'-GGA CCA CCC AGC TTC ATT ATG ACG AAG AAA C-3' (SEQ ID NO:142)

1436-18:

25 5'-GTT TCT TCG TCA TAA TGA AGC TGG GTG GTC C-3' (SEQ ID NO:143)

The following primer pairs were used to delete residues 22-31 of the human OPG gene, resulting in the production of a huOPG [32-401]-Fc fusion protein:

1436-27:

30 5'-GTG GAC CAC CCA GGA CGA AGA AAC CTC TC-3' (SEQ ID NO:144)

1436-28:

5'-GAG AGG TTT CTT CGT CCT GGG TGG TCC AC-3' (SEQ ID NO:145)

The following primer pairs were used to change the codon for tyrosine residue 28 to phenylalanine of the  
35 human OPG gene, resulting in the production of a huOPG [22-401]-Fc Y28F fusion protein:



1436-29:

5'-CGT TTC CTC CAA AGT TCC TTC ATT ATG AC-3' (SEQ ID NO:146)

1436-30:

5'-GTC ATA ATG AAG GAA CTT TGG AGG AAA CG-3' (SEQ ID NO:147)

5 The following primer pairs were used to change the codon for proline residue 26 to alanine of the human OPG gene, resulting in the production of a huOPG [22-401]-Fc P26A fusion protein:

1429-83:

10 5'-GGA AAC GTT TCC TGC AAA GTA CCT TCA TTA TG-3 (SEQ ID NO:148)

1429-84:

5'-CAT AAT GAA GGT ACT TTG CAG GAA ACG TTT CC-3' (SEQ ID NO:149)

Each resulting muOPG [22-401]-Fc plasmid containing the appropriate mutation was then  
15 transfected into human 293 cells, the mutant OPG-Fc fusion protein purified from conditioned media as described above. The biological activity of each protein was assessed the in vitro osteoclast forming assay described in Example 11.

20 EXAMPLE 8

Expression of OPG in E. coli

A. Bacterial Expression Vectors

pAMG21

The expression plasmid pAMG21 can be derived from  
25 the Amgen expression vector pCFM1656 (ATCC #69576) which in turn be derived from the Amgen expression vector system described in US Patent No. 4,710,473. The pCFM1656 plasmid can be derived from the described pCFM836 plasmid (Patent No. 4,710,473) by: (a)  
30 destroying the two endogenous NdeI restriction sites by end filling with T4 polymerase enzyme followed by blunt end ligation; (b) replacing the DNA sequence between the unique AatII and ClaI restriction sites containing the synthetic P<sub>L</sub> promoter with a similar fragment  
35 obtained from pCFM636 (patent No. 4,710,473) containing the PL promoter



AatII

5' CTAATTCCGCTCTCACCTACCAAACAATGCCCCCTGCAAAAAATAAATTCATAT-  
 3' TGCAGATTAAAGCGAGAGTGGATGGTTTGTACGGGGGACGTTTTTTATTTAAGTATA-

5 -AAAAACATACAGATAACCATCTGCGGTGATAAATTATCTCTGCGGGTGTGACATAAA-  
 -TTTTTTGTATGTCTATTGGTAGACGCCACTATTTAATAGAGACCGCCACAACGTATTT-

-TACCACTGGCGGTGATACTGAGCACAT 3' (SEQ ID NO:53)

-ATGGTGACCGCCACTATGACTCGTGTAGC5' (SEQ ID NO:54)

10

ClaI

and then (c) substituting the small DNA sequence  
 between the unique ClaI and KpnI restriction sites with  
 the following oligonucleotide:

5' CGATTTGATTCTAGAAGGAGGAATAACATATGGTTAACCGGTTGGAATTCGGTAC3'

15 (SEQ ID NO:48)

3' TAAACTAAGATCTTCCTCCTTATTGTATACCAATTGCGCAACCTTAAGC 5'

(SEQ ID NO:49)

ClaI

KpnI

The expression plasmid pAMG21 can then be derived  
 20 from pCFM1656 by making a series of site directed base  
 changes by PCR overlapping oligo mutagenesis and DNA  
 sequence substitutions. Starting with the BglII site  
 (plasmid bp # 180) immediately 5' to the plasmid  
 replication promoter PcopB and proceeding toward the  
 25 plasmid replication genes, the base pair changes are as  
 follows:

Table 4

	<u>pAMG21 bp #</u>	<u>bp in pCFM1656</u>	<u>bp changed to in pAMG21</u>
30	# 204	T/A	C/G
	# 428	A/T	G/C
	# 509	G/C	A/T
	# 617	- -	insert two G/C bp
	# 679	G/C	T/A
35	# 980	T/A	C/G
	# 994	G/C	A/T
	# 1004	A/T	C/G
	# 1007	C/G	T/A
	# 1028	A/T	T/A
40	# 1047	C/G	T/A
	# 1178	G/C	T/A
	# 1466	G/C	T/A
	# 2028	G/C	bp deletion
	# 2187	C/G	T/A



	# 2480	A/T	T/A
	# 2499-2502	AGTG TCAC	GTCA CAGT
5	# 2642	TCCGAGC AGGCTCG	7 bp deletion
10	# 3435	G/C	A/T
	# 3446	G/C	A/T
	# 3643	A/T	T/A

The DNA sequence between the unique AatII  
(position #4364 in pCFM1656) and SacII (position #4585  
15 in pCFM1656) restriction sites is substituted with the  
following DNA sequence:

```

[AatII sticky end]      5'   GCGTAACGTATGCATGGTCTCC-
(position #4358 in pAMG21) 3' TGCACGCATTGCATACGTACCAGAGG-

20 -CCATGCGAGAGTAGGGAAGTCCAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACT-
   -GGTACGCTCTCATCCCTTGACGGTCCGTAGTTATTTTGCCTTCCGAGTCAGCTTTCTGA-

   -GGGCTTTTCGTTTATCTGTTGTTGTGTCGGTGAACGCTCTCCTGAGTAGGACAAATCCGC-
   -CCCGGAAAGCAAAATAGACAACAACAGCCACTTGCGAGAGGACTCATCTGTTTAGGCG-

25 -CGGGAGCGGATTTGAACGTTGCGAAGCAACGCCCGGAGGGTGGCGGGCAGGACGCCCGC-
   -GCCCTCGCCTAAACTTGCAACGCTTCGTTGCCGGGCTCCACCGCCCGTCTGCGGGCG-

   -CATAAACTGCCAGGCATCAAATTAAGCAGAAGGCCATCCTGACGGATGGCCTTTTTCGGT-
30 -GTATTTGACGGTCCGTAGTTTAATTCGTCTTCCGGTAGGACTGCCTACCGGAAAAACGCA-

                                     AatII
   -TTCTACAAACTCTTTTGTGTTTATTTTCTAAATACATTCAAATATGGACGTCGTAATTAAAC-
   -AAGATGTTTGAGAAAACAAATAAAAAGATTTATGTAAGTTTATACCTGCAGCATGAATTG-

35 -TTTTAAAGTATGGGCAATCAATTGCTCCTGTTAAAAATTGCTTTAGAAATACTTTGGCAGC-
   -AAAATTTCATACCCGTTAGTTAACGAGGACAATTTTAACGAAATCTTTATGAAACCGTCG-

   -GGTTTGTGTTATTGAGTTTCATTTGCGCATTTGTTAAATGGAAAGTGACCGTGCGCTTAC-
40 -CCAAACAACATAACTCAAAGTAAACCGTAACCAATTTACCTTTCACTGGCACGCGAATG-

   -TACAGCCTAATATTTTGAATATCCCAAGAGCTTTTTCCTTCGCATGCCACGCTAAAC-
   -ATGTCGGATTATAAAAACCTTTATAGGTTCTCGAAAAAGGAAGCGTACGGGTGCGATTG-

45 -ATTCTTTTCTCTTTTGGTTAAATCGTTGTTGATTATTATTGCTATATTTATTTTTC-
   -TAAGAAAAAGAGAAAACCAATTTAGCAACAACTAAATAATAAACGATATAAATAAAAAG-

   -GATAATTATCAACTAGAGAAGGAACAATTAATGGTATGTTTCATACACGCATGTAAAAATA-
   -CTATTAATAGTTGATCTCTTCCTTGTTAATTACCATAACAAGTATGTGCGTACATTTTAT-

50 -AACTATCTATATAGTTGTCTTTCTCTGAATGTGCAAACTAAGCATTCCGAAGCCATTAT-
   -TTGATAGATATATCAACAGAAAGAGACTTACACGTTTGTGATTGTAAGGCTTCGGTAATA-

   -TAGCAGTATGAATAGGGAAGTAAACCGAGTATAAGACCTGATGATTTTCGTTCTTTTAA-
55 -ATCGTCATACTTATCCCTTTGATTTGGGTCACATTTCTGGACTACTAAAGCGAAGAAATT-

   -TTACATTTGGAGATTTTATTTTACAGCATTGTTTTCAAATATATTTCCAATTAATCGGTG-
   -AATGTAAACCTCTAAAAATAAATGTGCTAACAAGTTTATATAAGGTTAATTAGCCAC-

60 -AATGATTGGAGTTAGAATAATCTACTATAGGATCATATTTTATTAAATTAGCGTCATCAT-
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-TTACTAACCTCAATCTTATTAGATGATATCCTAGTATAAAATAATTTAATCGCAGTAGTA-  
 -AATATTGCCTCCATTTTTTAGGGTAATTATCCAGAATTGAAATATCAGATTTAACCATAG-  
 5 -TTATAACGGAGGTAAAAAATCCCATTAATAGGCTTAACTTTATAGTCTAAATTGGTATC-  
 -AATGAGGATAAATGATCGCGAGTAAATAATATTCACAATGTACCATTTTAGTCATATCAG-  
 -TTACTCCTATTTACTAGCGCTCATTTATTATAAGTGTACATGGTAAAATCAGTATAGTC-  
 10 -ATAAGCATTGATTAATATCATTATTGCTTCTACAGGCTTTAATTTTATTAATTATTCTGT-  
 -TATTCGTAACATAATTATAGTAATAACGAAGATGTCCGAAATTAATAATTAATAAGACA-  
 -AAGTGTCTGTCGGCATTTATGTCTTTCATACCCATCTCTTTATCCTTACCTATTGTTTGTG-  
 -TTCACAGCAGCCGTAAATACAGAAAGTATGGGTAGAGAAATAGGAATGGATAACAAACAG-  
 15 -GCAAGTTTTCGCGTGTATATATCATTAAAAACGGTAATAGATTGACATTTGATTTCTAATAA-  
 -CGTTCAAAACGCACATATATAGTAATTTTGCCATTATCTAACTGTAACTAAGATTATT-  
 -ATTGGATTTTTGTACACTATTATATCGCTTGAAATACAATTGTTTAAACATAAGTACCTG-  
 20 -TAACCTAAAAACAGTGTGATAATATAGCGAACTTTATGTTAACAAATTGTATTCATGGAC-  
 -TAGGATCGTACAGGTTTACGCAAGAAAATGGTTTGTATAGTCGATTAATCGATTTGATT-  
 -ATCCTAGCATGTCCAAATGCGTCTTTTACCAACAATATCAGCTAATTAGCTAAACTAA-  
 25 -CTAGATTTGTTTTAACTAATTAAGGAGGAATAACATATGGTTAACCGGTTGGAATTCGA-  
 -GATCTAAACAAAATTGATTAATTTCTCTTATTGTATACCAATTGCGCAACCTTAAGCT-  
 SacII  
 -GCTCACTAGTGTGACCTGCAGGTACCATGGAAGCTTACTCGAGGATCCGCGGAAAGAA-  
 30 -CGAGTGATCACAGCTGACGTCCCATGGTACCTTCGAATGAGTCCTAGGCGCCTTTCTT-  
 -GAAGAAGAAGAAGAAAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGCAATA-  
 -CTTCTTCTTCTTCTTTTGGGCTTTCTTTCGACTCAACCGACGACGGTGGCGACTCGTTAT-  
 35 -ACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTTTGCTGAAAGGAGG-  
 -TGATCGTATTGGGAACCCCGGAGATTGCCCAGAACTCCCCAAAAACGACTTTCTCTCC-  
 -AACCGCTCTTCACGCTCTTCACGC 3' [SacII sticky end] (SEQ ID NO:50)  
 -TTGGCGAGAAGTGCGAGAAGTG 5' (position #5904 in pAMG21)  
 (SEQ ID NO:46)

40 During the ligation of the sticky ends of this  
 substitution DNA sequence, the outside AatII and SacII  
 sites are destroyed. There are unique AatII and SacII  
 sites in the substituted DNA.

#### 45 pAMG22-His

The expression plasmid pAMG22-His can be derived  
 from the Amgen expression vector pAMG22 by substituting  
 the small DNA sequence between the unique NdeI ( #4795)  
 and EcoRI ( #4818) restriction sites of pAMG22 with the  
 50 following oligonucleotide duplex:

NdeI                      NheI                      EcoRI  
 5' TATGAAACATCATCACCATCACCATCATGCTAGCGTTAACGCGTTGG 3'  
 (SEQ ID NO:51)  
 3' ACTTTGTAGTAGTGGTAGTGGTAGTACGATCGCAATTGCGCAACCTTAA 5'



(SEQ ID NO:52)

MetLysHisHisHisHisHisHisHisAlaSerValAsnAlaLeuGlu

(SEQ ID NO:168)

pAMG22

5       The expression plasmid pAMG22 can be derived from  
the Amgen expression vector pCFM1656 (ATCC #69576)  
which in turn be derived from the Amgen expression  
vector system described in US Patent No. 4,710,473  
granted December 1, 1987. The pCFM1656 plasmid can be  
10       derived from the described pCFM836 plasmid (Patent No.  
4,710,473) by: (a) destroying the two endogenous NdeI  
restriction sites by end filling with T4 polymerase  
enzyme followed by blunt end ligation; (b) replacing  
the DNA sequence between the unique AatII and ClaI  
15       restriction sites containing the synthetic PL promoter  
with a similar fragment obtained from pCFM636 (patent  
No. 4,710,473) containing the PL promoter

AatII

5'       CTAATTCGCTCTCACCTACCAAACAATGCCCCCTGCAAAAAATAAATTCATAT-  
20       3'TGCAGATTAAAGCGAGAGTGGATGGTTTGTGTACGGGGGACGTTTTTTATTTAAGTATA-

-AAAAACATACAGATAACCATCTGCGGTGATAAATTATCTCTGGCGGTGTTGACATAAA-  
-TTTTTTGTATGTCTATTGGTAGACGCCACTATTTAATAGAGACCGCCACAACGTATTT-

25       -TACCACTGGCGGTGATACTGAGCACAT 3' (SEQ ID NO:53)

-ATGGTGACCGCCACTATGACTCGTGTAGC5' (SEQ ID NO:54)

ClaI

and then (c) substituting the small DNA sequence  
between the unique ClaI and KpnI restriction sites with  
30       the following oligonucleotide:

5' CGATTTGATTCTAGAAGGAGGAATAACATATGGTTAACGCGTTGGAATTCGGTAC 3'  
(SEQ ID NO:55)

3' TAACTAAGATCTTCCTCCTTATTGTATACCAATTGCGCAACCTTAAGC 5'  
(SEQ ID NO:56)

35       ClaI

KpnI



The expression plasmid pAMG22 can then be derived from pCFM1656 by making a series of site directed base changes by PCR overlapping oligo mutagenesis and DNA sequence substitutions. Starting with the BglII site (plasmid bp # 180) immediately 5' to the plasmid replication promoter PcopB and proceeding toward the plasmid replication genes, the base pair changes are as follows:

Table 5

	<u>pAMG22 bp #</u>	<u>bp in pCFM1656</u>	<u>bp changed to in pAMG22</u>
	# 204	T/A	C/G
	# 428	A/T	G/C
15	# 509	G/C	A/T
	# 617	- -	insert two G/C bp
	# 679	G/C	T/A
	# 980	T/A	C/G
20	# 994	G/C	A/T
	# 1004	A/T	C/G
	# 1007	C/G	T/A
	# 1028	A/T	T/A
	# 1047	C/G	T/A
25	# 1178	G/C	T/A
	# 1466	G/C	T/A
	# 2028	G/C	bp deletion
	# 2187	C/G	T/A
	# 2480	A/T	T/A
30	# 2499-2502	AGTG TCAC	GTCA CAGT
	# 2642	TCCGAGC AGGCTCG	7 bp deletion
35	# 3435	G/C	A/T
	# 3446	G/C	A/T
	# 3643	A/T	T/A

40 The DNA sequence between the unique AatII (position #4364 in pCFM1656) and SacII (position #4585 in pCFM1656) restriction sites is substituted with the following DNA sequence:

[AatII sticky end] (position #4358 in pAMG22)

45



5' GCGTAACGTATGCATGGTCTCCCATGCGAGAGTAGGGAAGTCCAGGCATCAA-  
 3' TGCACGCATTGCATACGTACCAGAGGGGTACGCTCTCATCCCTTGACGGTCCGTAGTT-  
 -ATAAAACGAAAGGCTCAGTCGAAAGACTGGGCCCTTTCGTTTTATCTGTTGTTTGTCCGGTG-  
 5 -TATTTTGCCTTCCGAGTCAGCTTTCGACCCGGAAGCAAAATAGACAACAAACAGCCAC-  
 -AACGCTCTCCTGAGTAGGACAAATCCGCCGGGAGCGGATTTGAACGTTGCGAAGCAACGG-  
 10 -TTGCGAGAGGACTCATCTGTTTAGGCGGCCCTCGCCTAAACTTGCAACGCTTCGTTGCC-  
 -CCCGGAGGGTGGCGGGCAGGACGCCGCCATAAACTGCCAGGCATCAAATTAAGCAGAAG-  
 -GGGCCTCCACCGCCGCTCTGCGGGCGGTATTTGACGGTCCGTAGTTTAATTCGTCTTC-  
 -GCCATCCTGACGGATGGCCTTTTTCGCTTCTACAACTCTTTTGTATTATTTTCTAAAT-  
 15 -CGGTAGGACTGCCTACCGAAAAACGCAAGATGTTTGAGAAAAACAAATAAAAAGATTTA-  
 AatII  
 -ACATTCAAATATGACGCTCTCATAATTTTAAAAAATTCATTTGACAAATGCTAAAATTC-  
 -TGTAAGTTTATACCTGCAGAGTATTAAAAATTTTAAAGTAACTGTTTACGATTTTAAG-  
 20 -TTGATTAAATATTCTCAATTGTGAGCGCTCACAATTTATCGATTTGATTCTAGATTTGTTT-  
 -AACTAATTATAAGAGTTAACAACCTCGCGAGTGTTAAATAGCTAAACTAAGATCTAAACTCA-  
 -TAACTAATTAAAGGAGGAATAACATATGGTTAACCGGTTGGAATTCGAGCTCACTAGTGT-  
 25 -ATTGATTAAATTTCTCTTATTGTATACCAATTGCGCAACCTTAAGCTCGAGTGATCACA-  
 SacII  
 -CGACCTGCAGGGTACCATGGAAGCTTACTCGAGGATCCGCGGAAAGAAGAAGAAGAA-  
 30 -GCTGGACGTCCCATGGTACCTTCGAATGAGCTCCTAGGCGCCTTCTTCTTCTTCTTCTT-  
 -GAAAGCCCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTGAGCAATAACTAGCATAACC-  
 -CTTTCGGGCTTTCCTTCGACTCAACCGACGACGGTGGCGACTCGTTATTGATCGTATTGG-  
 -CCTTGGGGCTCTAAACGGGTCTTGAGGGGTTTTTGTCTGAAAGGAGGAACCGCTCTTCA-  
 35 -GGAACCCCGGAGATTTGCCCAGAACTCCCAAAAAACGACTTTCCTCCTTGGCGAGAAGT-  
 -CGCTCTTCACGC 3' (SEQ ID NO:58)  
 -GCGAGAAGTG 5' (SEQ ID NO:57)

40 [SacII sticky end] (position #5024 in pAMG22)  
 During the ligation of the sticky ends of this  
 substitution DNA sequence, the outside AatII and SacII  
 sites are destroyed. There are unique AatII and SacII  
 sites in the substituted DNA.

#### 45 B. Human OPG Met[32-401]

In the example, the expression vector used was  
 pAMG21, a derivative of pCFM1656 (ATCC accession no.  
 69576) which contains appropriate restriction sites for  
 insertion of genes downstream from the lux PR promoter.  
 50 (See U.S. Patent No. 5,169,318 for description of the  
lux expression system). The host cell used was GM120  
 (ATCC accession no. 55764). This host has the lacIQ  
 promoter and lacI gene integrated into a second site in



the host chromosome of a prototrophic E. coli K12 host. Other commonly used E. coli expression vectors and host cells are also suitable for expression.

A DNA sequence coding for an N-terminal methionine and amino acids 32-401 of the human OPG polypeptide was placed under control of the luxPR promoter in the plasmid expression vector pAMG21 as follows. To accomplish this, PCR using oligonucleotides #1257-20 and #1257-19 as primers was performed using as a template plasmid pRCCMV-Hu OPG DNA containing the human OPG cDNA and thermocycling for 30 cycles with each cycle being: 94°C for 20 seconds, followed by 37°C for 30 seconds, followed by 72°C for 30 seconds. The resulting PCR sample was resolved on an agarose gel, the PCR product was excised, purified, and restricted with KpnI and BamHI restriction endonucleases and purified. Synthetic oligonucleotides #1257-21 and #1257-22 were phosphorylated individually using T4 polynucleotide kinase and ATP, and were then mixed together, heated at 94°C and allowed to slow cool to room temperature to form an oligonucleotide linker duplex containing NdeI and KpnI sticky ends. The phosphorylated linker duplex formed between oligonucleotides #1257-21 and #1257-22 containing NdeI and KpnI cohesive ends (see Figure 14A) and the KpnI and BamHI digested and purified PCR product generated using oligo primers #1257-20 and #1257-19 (see above) was directionally inserted between two sites of the plasmid vector pAMG21, namely the NdeI site and BamHI site, using standard recombinant DNA methodology (see Figure 14A and sequences below). The synthetic linker utilized E. coli codons and provided for a N-terminal methionine.

Two clones were selected and plasmid DNA isolated, and the human OPG insert was subsequently DNA sequence confirmed. The resulting pAMG21 plasmid containing



amino acids 32-401 of the human OPG polypeptide immediately preceded in frame by a methionine is referred to as pAMG21-huOPG met[32-401] or pAMG21-huOPG met[32-401].

5 Oligo#1257-19:

5'-TACGCACTGGATCCTTATAAGCAGCTTATTTTACTGATTGGAC-3'  
(SEQ ID NO:59)

Oligo#1257-20:

5'-GTCCTCCTGGTACCTACCTAAAACAAC-3' (SEQ ID NO:60)

10 Oligo#1257-21:

5'-TATGGATGAAGAACTTCTCATCAGCTGCTGTGTGATAAATGTCCGCCGGGTAC -3'  
(SEQ ID NO:61)

Oligo#1257-22:

5'-CCGGCGGACATTTATCACACAGCAGCTGATGAGAAGTTCTTCATCCA-3'  
15 (SEQ ID NO:47)

Cultures of pAMG21-huOPG met[32-401] in *E. coli* GM120 in 2XYT media containing 20 µg/ml kanamycin were incubated at 30°C prior to induction. Induction of huOPG met[32-401] gene product expression from the luxPR promoter was achieved following the addition of  
20 the synthetic autoinducer N-(3-oxohexanoyl)-DL-homoserine lactone to the culture media to a final concentration of 30 ng/ml and cultures were incubated at either 30°C or 37°C for a further 6 hours. After 6  
25 hours, the bacterial cultures were examined by microscopy for the presence of inclusion bodies and were then pelleted by centrifugation. Refractile inclusion bodies were observed in induced cultures indicating that some of the recombinant huOPG met[32-  
30 401] gene product was produced insolubly in *E. coli*.

Some bacterial pellets were resuspended in 10mM Tris-HCl/pH8, 1mM EDTA and lysed directly by addition of 2X Laemlli sample buffer to 1X final, and β-mercaptoethanol to 5% final concentration, and analyzed  
35 by SDS-PAGE. A substantially more intense coomassie stained band of approximately 42kDa was observed on a



SDS-PAGE gel containing total cell lysates of 30°C and 37°C induced cultures versus lane 2 which is a total cell lysate of a 30°C uninduced culture (Figure 14B). The expected gene product would be 370 amino acids in length and have an expected molecular weight of about 42.2 kDa.

Following induction at 37 °C for 6 hours, an additional culture was pelleted and either processed for isolation of inclusion bodies (see below) or processed by microfluidizing. The pellet processed for microfluidizing was resuspended in 25mM Tris-HCl/pH8, 0.5M NaCl buffer and passed 20 times through a Microfluidizer Model 1108 (Microfluidics Corp.) and collected. An aliquot was removed of the collected sample (microfluidized total lysate), and the remainder was pelleted at 20,000 x g for 20 minutes. The supernatant following centrifugation was removed (microfluidized soluble fraction) and the pellet resuspended in a 25mM Tris-HCl/pH8, 0.5M NaCl, 6M urea solution (microfluidized insoluble fraction). To an aliquot of either the total soluble, or insoluble fraction was added to an equal volume of 2X Laemalli sample buffer and  $\beta$ -mercaptoethanol to 5% final concentration. The samples were then analyzed by SDS-PAGE. A significant amount of recombinant huOPG met[32-401] gene product appeared to be found in the insoluble fraction.

To purify the recombinant protein, inclusion bodies were purified as follows: Bacterial cells were separated from media by density gradient centrifugation in a Beckman J-6B centrifuge equipped with a JS-4.2 rotor at 4,900 x g for 15 minutes at 4°C. The bacterial pellet was resuspended in 5 ml of water and then diluted to a final volume of 10 ml with water. This suspension was transferred to a stainless steel cup



cooled in ice and subjected to sonic disruption using a Branson Sonifier equipped with a standard tip (power setting=5, duty cycle=95%, 80 bursts). The sonicated cell suspension was centrifuged in a Beckman Optima TLX  
5 ultracentrifuge equipped with a TLA 100.3 rotor at 195,000 x g for 5 to 10 minutes at 23°C. The supernatant was discarded and the pellet rinsed with a stream of water from a squirt bottle. The pellets were collected by scraping with a micro spatula and  
10 transferred to a glass homogenizer (15 ml capacity). Five ml of Percoll solution (75% liquid Percoll, 0.15 M sodium chloride) was added to the homogenizer and the contents are homogenized until uniformly suspended. The volume was increased to 19.5 ml by the addition of  
15 Percoll solution, mixed, and distributed into 3 Beckman Quick-Seal tubes (13 x 32 mm). Tubes were sealed according to manufacturers instructions. The tubes were spun in a Beckman TLA 100.3 rotor at 23°C, 20,000 rpm (21,600 x g), 30 minutes. The tubes were examined for  
20 the appropriate banding pattern. To recover the refractile bodies, gradient fractions were recovered and pooled, then diluted with water. The inclusion bodies were pelleted by centrifugation, and the protein concentration estimated following SDS-PAGE.

25 An aliquot of inclusion bodies isolated as described below was dissolved into 1X Laemmli sample buffer with 5%  $\beta$ -mercaptoethanol and resolved on a SDS-PAGE gel and the isolated inclusion bodies provide a highly purified recombinant huOPG[32-401] gene product.  
30 The major ~42 kDa band observed after resolving inclusion bodies on a SDS-polyacrylamide gel was excised from a separate gel and the N-terminal amino acid sequence determined essentially as described (Matsudaira et al. J. Biol. Chem. 262, 10-35 (1987)).  
35 The following sequence was determined after 19 cycles:



NH<sub>2</sub> -MDEETSHQLLCDKCPPGTY-COOH (SEQ ID NO:62)

This sequence was found to be identical to the first 19 amino acids encoded by the pAMG21 Hu-OPG met[32-401] expression vector, produced by a methionine residue  
5 provided by the bacterial expression vector.



C. Human OPG met[22-401]

A DNA sequence coding for an N-terminal methionine and amino acids 22 through 401 of human OPG was placed under control of the luxPR promoter in a prokaryotic plasmid expression vector pAMG21 as follows. Isolated plasmid DNA of pAMG21-huOPG met[32-401] (see Section B) was cleaved with KpnI and BamHI restriction endonucleases and the resulting fragments were resolved on an agarose gel. The B fragment (about 1064 bp fragment) was isolated from the gel using standard methodology. Synthetic oligonucleotides (oligos) #1267-06 and #1267-07 were phosphorylated individually and allowed to form an oligo linker duplex, which contained NdeI and KpnI cohesive ends, using methods described in Section B. The synthetic linker duplex utilized E. coli codons and provided for an N-terminal methionine. The phosphorylated oligo linker containing NdeI and KpnI cohesive ends and the isolated about 1064 bp fragment of pAMG21-huOP met[32-401] digested with KpnI and BamHI restriction endonucleases were directionally inserted between the NdeI and BamHI sites of pAMG21 using standard recombinant DNA methodology. The ligation mixture was transformed into E. coli host 393 by electroporation utilizing the manufacturer's protocol. Clones were selected, plasmid DNA was isolated, and DNA sequencing was performed to verify the DNA sequence of the huOPG-met[22-401] gene.

## Oligo #1267-06:

5'-TAT GGA AAC TTT TCC TCC AAA ATA TCT TCA TTA TGA TGA AGA AAC TTC  
TCA TCA GCT GCT GTG TGA TAA ATG TCC GCC GGG TAC-3'  
(SEQ ID NO:63)

## Oligo #1267-07:

5'-CCG GCG GAC ATT TAT CAC ACA GCA GCT GAT GAG AAG TTT CTT CAT  
CAT AAT GAA GAT ATT TTG GAG GAA AAG TTT CCA-3'  
(SEQ ID NO:64)



Cultures of pAMG21-huOPG-met[22-401] in *E. coli* host 393 were placed in 2XYT media containing 20 µg/ml kanamycin and were incubated at 30°C prior to induction. Induction of recombinant gene product expression from the luxPR promoter of vector pAMG21 was achieved following the addition of the synthetic autoinducer N-(3-oxohexanoyl)-DL-homoserine lactone to the culture media to a final concentration of 30 ng/ml and incubation at either 30°C or 37°C for a further 6 hours. After 6 hours, bacterial cultures were pelleted by centrifugation (=30°C I+6 or 37°C I+6). Bacterial cultures were also either pelleted just prior to induction (=30°C PreI) or alternatively no autoinducer was added to a separate culture which was allowed to incubate at 30°C for a further 6 hours to give an uninduced (UI) culture (=30°C UI). Bacterial pellets of either 30°C PreI, 30°C UI, 30°C I+6, or 37°C I+6 cultures were resuspended, lysed, and analyzed by SDS-polyacrylamide gel electrophoresis (PAGE) as described in Section B. Polyacrylamide gels were either stained with coomassie blue and/or Western transferred to nitrocellulose and immunoprobed with rabbit anti-mu OPG-Fc polyclonal antibody as described in Example 10. The level of gene product following induction compared to either an uninduced (30°C UI) or pre-induction (30°C PreI) sample.

#### D. Murine OPG met[22-401]

A DNA sequence coding for an N-terminal methionine and amino acids 22 through 401 of the murine (mu) OPG (OPG) polypeptide was placed under control of the luxPR promoter in a prokaryotic plasmid expression vector pAMG21 as follows. PCR was performed using oligonucleotides #1257-16 and #1257-15 as primers, plasmid pRcCMV-Mu OPG DNA as a template and thermocycling conditions as described in Section B. The PCR product was purified and cleaved with KpnI and



BamHI restriction endonucleases as described in Section B. Synthetic oligos #1260-61 and #1260-82 were phosphorylated individually and allowed to form an oligo linker duplex with NdeI and KpnI cohesive ends using methods described in Section B. The synthetic linker duplex utilized E. coli codons and provided for an N-terminal methionine. The phosphorylated linker duplex formed between oligos #1260-61 and #1260-82 containing NdeI and KpnI cohesive ends and the KpnI and BamHI digested and purified PCR product generated using oligo primers #1257-16 and #1257-15 were directionally inserted between the NdeI and BamHI sites of pAMG21 using standard methodology. The ligation mixture was transformed into E. coli host 393 by electroporation utilizing the manufacturer's protocol. Clones were selected, plasmid DNA was isolated, and DNA sequencing was performed to verify the DNA sequence of the MuOPG met[22-401] gene.

Expression of recombinant muOPG met[22-401] polypeptide from cultures of 393 cells harboring plasmid pAMG21-MuOPG met[22-401] following induction was determined using methods described in Section C.

Oligo #1257-15:

5'-TAC GCA CTG GAT CCT TAT AAG CAG CTT ATT TTC ACG GAT TGA AC-3'  
(SEQ ID NO:65)

Oligo #1257-16:

5'-GTG CTC CTG GTA CCT ACC TAA AAC AGC ACT GCA CAG TG-3'  
(SEQ ID NO:66)

Oligo #1260-61:

5'-TAT GGA AAC TCT GCC TCC AAA ATA CCT GCA TTA CGA TCC GGA AAC TGG  
TCA TCA GCT GCT GTG TGA TAA ATG TGC TCC GGG TAC-3'  
(SEQ ID NO:67)

Oligo #1260-82:

5'-CCG GAG CAC ATT TAT CAC ACA GCA GCT GAT GAC CAG TTT CCG GAT CGT  
AAT GCA GGT ATT TTG GAG GCA GAG TTT CCA-3'  
(SEQ ID NO:68)



E. Murine OPG met[32-401]

A DNA sequence coding for an N-terminal methionine and amino acids 32 through 401 of murine OPG was placed under control of the luxPR promoter in a prokaryotic  
5 plasmid expression vector pAMG21 as follows. To accomplish this, Synthetic oligos #1267-08 and #1267-09 were phosphorylated individually and allowed to form an oligo linker duplex using methods described in Section B. The synthetic linker duplex utilized E. coli codons  
10 and provided for an N-terminal methionine. The phosphorylated linker duplex formed between oligos #1267-08 and #1267-09 containing NdeI and KpnI cohesive ends, and the KpnI and BamHI digested and purified PCR product described earlier (see Section D), was  
15 directionally inserted between the NdeI and BamHI sites of pAMG21 using standard methodology. The ligation mixture was transformed into E. coli host 393 by electroporation utilizing the manufacturer's protocol. Clones were selected, plasmid DNA was isolated, and DNA  
20 sequencing was performed to verify the DNA sequence of the muOPG-met[32-401] gene.

Expression of recombinant muOPG-met [32-401] polypeptide from cultures of 393 cells harboring the pAMG21 recombinant plasmid following induction was  
25 determined using methods described in Section C.

## Oligo #1267-08:

5'-TAT GGA CCC AGA AAC TGG TCA TCA GCT GCT GTG TGA TAA ATG TGC TCC  
GGG TAC-3' (SEQ ID NO:69)

## Oligo #1267-09:

30 5'-CCG GAG CAC ATT TAT CAC ACA GCA GCT GAT GAC CAG TTT CTG GGT  
CCA-3' (SEQ ID NO:70)

E. Murine OPG met-lys[22-401]

A DNA sequence coding for an N-terminal methionine followed by a lysine residue and amino acids 22 through  
35 401 of murine OPG was placed under control of the lux PR promoter in prokaryotic expression vector pAMG21 as



follows. Synthetic oligos #1282-95 and #1282-96 were phosphorylated individually and allowed to form an oligo linker duplex using methods described in Section B. The synthetic linker duplex utilized E. coli codons and provided for an N-terminal methionine. The phosphorylated linker duplex formed between oligos #1282-95 and #1282-96 containing NdeI and KpnI cohesive ends and the KpnI and BamHI digested and purified PCR product described in Section D was directionally inserted between the NdeI and BamHI sites in pAMG21 using standard methodology. The ligation mixture was transformed into E. coli host 393 by electroporation utilizing the manufacturer's protocol. Clones were selected, plasmid DNA was isolated, and DNA sequencing was performed to verify the DNA sequence of the MuOPG-Met-Lys[22-401] gene.

Expression of recombinant MuOPG Met-Lys[22-401] polypeptide from transformed 393 cells harboring the recombinant pAMG21 plasmid following induction was determined using methods described in Section C.

Oligo #1282-95:

5'-TAT GAA AGA AAC TCT GCC TCC AAA ATA CCT GCA TTA CGA TCC GGA AAC  
TGG TCA TCA GCT GCT GTG TGA TAA ATG TGC TCC GGG TAC-3'  
(SEQ ID NO:71)

Oligo #1282-96:

5'-CCG GAG CAC ATT TAT CAC ACA GCA GCT GAT GAC CAG TTT CCG GAT CGT  
AAT GCA GGT ATT TTG GAG GCA GAG TTT CTT TCA-3' (SEQ ID NO:72)  
G. Murine OPG met-lys-(his)<sub>7</sub>[22-401]

A DNA sequence coding for N-terminal residues Met-Lys-His-His-His-His-His-His (=MKH) followed by amino acids 22 through 401 of Murine OPG was placed under control of the lux PR promoter in prokaryotic expression vector pAMG21 as follows. PCR was performed using oligonucleotides #1300-50 and #1257-15 as primers and plasmid pAMG21-muOPG-met[22-401] DNA as template. Thermocycling conditions were as described in Section



B. The resulting PCR sample was resolved on an agarose gel, the PCR product was excised, purified, cleaved with NdeI and BamHI restriction endonucleases and purified. The NdeI and BamHI digested and purified PCR product generated using oligo primers #1300-50 and #1257-15 was directionally inserted between the NdeI and BamHI sites of pAMG21 using standard DNA methodology. The ligation mixture was transformed into E. coli host 393 by electroporation utilizing the manufacturer's protocol. Clones were selected, plasmid DNA was isolated, and DNA sequencing performed to verify the DNA sequence of the muOPG-MKH[22-401] gene.

Expression of recombinant MuOPG-MKH[22-401] polypeptide from transformed 393 cultures harboring the recombinant pAMG21 plasmid following induction was determined using methods described in Section C.

Oligo #1300-50:

5'-GTT CTC CTC ATA TGA AAC ATC ATC ACC ATC ACC ATC ATG AAA CTC TGC CTC CAA AAT ACC TGC ATT ACG AT-3' (SEQ ID NO:73)

Oligo #1257-15: see Section D

H. Murine OPG met-lys[22-401](his)<sub>7</sub>

A DNA sequence coding for a N-terminal met-lys, amino acids 22 through 401 murine OPG, and seven histidine residues following amino acid 401 (=muOPG MK[22-401]-H<sub>7</sub>), was placed under control of the lux PR promoter in prokaryotic expression vector pAMG21 as follows. PCR was performed using oligonucleotides #1300-49 and #1300-51 as primers and pAMG21-muOPG met[22-401] DNA as template. Thermocycling conditions were as described in Section B. The resulting PCR sample was resolved on an agarose gel, the PCR product was excised, purified, restricted with NdeI and BamHI restriction endonucleases, and purified. The NdeI and BamHI digested and purified PCR product was directionally inserted between the NdeI and BamHI sites in pAMG21 using standard methodology. The ligation was



transformed into E. coli host 393 by electroporation utilizing the manufacturer's protocol. Clones were selected, plasmid DNA was isolated, and DNA sequencing was performed to verify the DNA sequence of the muOPG  
5 MK[22-401]-H7 gene.

Expression of the recombinant muOPG MK-[22-401]-H7 polypeptide from a transformed 393 cells harboring the recombinant pAMG21 plasmid following induction was determined using methods described in Section C.

10 Oligo #1300-49:

5'-GTT CTC CTC ATA TGA AAG AAA CTC TGC CTC CAA AAT ACC TGC A-3'  
(SEQ ID NO:74)

Oligo #1300-51:

5'-TAC GCA CTG GAT CCT TAA TGA TGG TGA TGG TGA TGA TGT AAG CAG CTT  
15 ATT TTC ACG GAT TGA ACC TGA TTC CCT A-3' (SEQ ID NO:75)

I. Murine OPG met[27-401]

A DNA sequence coding for a N-terminal methionine and amino acids 27 through 401 of murine OPG was placed under control of the lux PR promoter of prokaryotic  
20 expression vector pAMG21 as follows. PCR was performed with oligonucleotides #1309-74 and #1257-15 as primers and plasmid pAMG21-muOPG-met[22-401] DNA as template. Thermocycling conditions were as described in Section B. The resulting PCR sample was resolved on an agarose  
25 gel, the PCR product was excised, purified, cleaved with NdeI and BamHI restriction endonucleases, and purified. The NdeI and BamHI digested and purified PCR product was directionally inserted between the NdeI and BamHI sites of pAMG21 using standard methodology. The  
30 ligation mixture was transformed into E. coli host 393 by electroporation utilizing the manufacturer's protocol. Clones were selected, plasmid DNA was isolated, and DNA sequencing was performed to verify the DNA sequence of the muOPG-met[27-401] gene.

35 Expression of recombinant muOPG-met[27-401] polypeptide from a transfected 393 culture harboring



the recombinant pAMG21 plasmid following induction was determined using methods described in Section C.

Oligo#1309-74:

5'-GTT CTC CTC ATA TGA AAT ACC TGC ATT ACG ATC CGG AAA CTG GTC AT-  
3' (SEQ ID NO:76)

Oligo#1257-15: See Section D

J. Human OPG met[27-401]

A DNA sequence coding for a N-terminal methionine and amino acids 27 through 401 of human OPG was placed under control of the lux PR promoter of prokaryotic expression vector pAMG21 as follows. PCR was performed using oligonucleotides #1309-75 and #1309-76 as primers and plasmid pAMG21-huOPG-met[22-401] DNA as template. Thermocycling conditions were as described in Section B. The resulting PCR sample was resolved on an agarose gel, the PCR product was excised, purified, restricted with AseI and BamHI restriction endonucleases, and purified. The AseI and BamHI digested and purified PCR product above was directionally inserted between the NdeI and BamHI sites of pAMG21 using standard methodology. The ligation mixture was transformed into E. coli host 393 by electroporation utilizing the manufacturer's protocol. Clones were selected, plasmid DNA was isolated, and DNA sequencing was performed to verify the DNA sequence of the huOPG-met[27-401] gene.

Expression of the recombinant huOPG-met[27-401] polypeptide following induction of from transfected 393 cells harboring the recombinant pAMG21 plasmid was determined using methods described in Section C.

Oligo #1309-75:

5'-GTT CTC CTA TTA ATG AAA TAT CTT CAT TAT GAT GAA GAA ACT T-3'  
(SEQ ID NO:77)

Oligo #1309-76:

5'-TAC GCA CTG GAT CCT TAT AAG CAG CTT ATT TTT ACT GAT T-3'  
(SEQ ID NO:78)



K. Murine OPG met[22-180]

A DNA sequence coding for a N-terminal methionine and amino acids 22 through 180 of murine OPG was placed under control of the lux PR promoter of prokaryotic expression vector pAMG21 as follows. PCR was performed with oligonucleotides #1309-72 and #1309-73 as primers and plasmid pAMG21-muOPG-met[22-401] DNA as template. Thermocycling conditions were as described in Section B. The resulting PCR sample was resolved on an agarose gel, the PCR product was excised, purified, restricted with NdeI and BamHI restriction endonucleases, and purified. The NdeI and BamHI digested and purified PCR product above was directionally inserted between the NdeI and BamHI sites of pAMG21 using standard methodology. The ligation was transformed into E. coli host 393 by electroporation utilizing the manufacturer's protocol. Clones were selected, plasmid DNA was isolated, and DNA sequencing was performed to verify the DNA sequence of the muOPG-met[22-180] gene.

Expression of recombinant muOPG-met[22-180] polypeptide from transformed 393 cultures harboring the recombinant pAMG21 plasmid following induction was determined using methods described in Section C.

Oligo #1309-72:

5'-GTT CTC CTC ATA TGG AAA CTC TGC CTC CAA AAT ACC TGC A-3'  
(SEQ ID NO:79)

Oligo #1309-73:

5'-TAC GCA CTG GAT CCT TAT GTT GCA TTT CCT TTC TGA ATT AGC A-3'  
(SEQ ID NO:80)

L. Murine OPG met[27-180]

A DNA sequence coding for a N-terminal methionine and amino acids 27 through 180 of murine OPG was placed under the control of the lux PR promoter of prokaryotic expression vector pAMG21 as follows. PCR was performed using oligonucleotides #1309-74 (see Section I) and #1309-73 (see Section K) as primers and plasmid pAMG21-



muOPG met[22-401] DNA as template. Thermocycling conditions were as described in Section B. The resulting PCR sample was resolved on an agarose gel, the PCR product excised, purified, restricted with NdeI and BamHI restriction endonucleases, and purified. The NdeI and BamHI digested and purified PCR product above was directionally inserted between the NdeI and BamHI sites in pAMG21 using standard methodology. The ligation mixture was transformed into E. coli host 393 by electroporation utilizing the manufacturer's protocol. Clones were selected, plasmid DNA was isolated, and DNA sequencing was performed to verify the DNA sequence of the muOPG met[27-180] gene.

Expression of recombinant muOPG met[27-180] polypeptide from cultures of transformed 393 cells harboring the recombinant pAMG21 plasmid following induction was determined using methods described in Section C.

M. Murine OPG met[22-189] and met[22-194]

A DNA sequence coding for a N-terminal methionine and either amino acids 22 through 189, or 22 through 194 of murine OPG was placed under control of the lux PR promoter of prokaryotic expression vector pAMG21 as follows. The pair of synthetic oligonucleotides #1337-92 and #1337-93 (=muOPG-189 linker) or #1333-57 and #1333-58 (=muOPG-194 linker) were phosphorylated individually and allowed to form an oligo linker duplex pair using methods described in Section B. Purified plasmid DNA of pAMG21-muOPG-met[22-401] was cleaved with KpnI and BspEI restriction endonucleases and the resulting DNA fragments were resolved on an agarose gel. The ~413 bp B fragment was isolated using standard recombinant DNA methodology. The phosphorylated oligo linker duplexes formed between either oligos #1337-92 and #1337-93 (muOPG-189 linker) or oligos #1333-57 and #1333-58 (muOPG-194 linker) containing BspEI and BamHI



cohesive ends, and the isolated ~413 bp B fragment of plasmid pAMG21-muOPG-met[22-401] digested with KpnI and BspEI restriction endonucleases above, was directionally inserted between the KpnI and BamHI sites of pAMG21-muOPG met[22-401] using standard methodology. Each ligation mixture was transformed into *E. coli* host 393 by electroporation utilizing the manufacturer's protocol. Clones were selected, plasmid DNA was isolated, and DNA sequencing was performed to verify the DNA sequence of either the muOPG-met[22-189] or muOPG-met[22-194] genes.

Expression of recombinant muOPG-met[22-189] and muOPG-met[22-194] polypeptides from recombinant pAMG21 plasmids transformed into 393 cells was determined using methods described in Section C.

Oligo #1337-92:

5'-CCG GAA ACA GAT AAT GAG-3' (SEQ ID NO:81)

Oligo #1337-93:

5'-GAT CCT CAT TAT CTG TTT-3' (SEQ ID NO:82)

Oligo #1333-57:

5'-CCG GAA ACA GAG AAG CCA CGC AAA AGT AAG-3'  
(SEQ ID NO:83)

Oligo #1333-58:

5'-GAT CCT TAC TTT TGC GTG GCT TCT CTG TTT-3'  
(SEQ ID NO:84)

N. Murine OPG met[27-189] and met[27-194]

A DNA sequence coding for a N-terminal methionine and either amino acids 27 through 189, or 27 through 194 of murine OPG was placed under control of the lux PR promoter of prokaryotic expression vector pAMG21 as follows. Phosphorylated oligo linkers either "muOPG-189 linker" or "muOPG-194 linker" (see Section M) containing BspEI and BamHI cohesive ends, and the isolated ~413 bp B fragment of plasmid pAMG21-muOPG-met[22-401] digested with KpnI and BspEI restriction endonucleases were directionally inserted between the



KpnI and BamHI sites of plasmid pAMG21-muOPG-met[27-401] using standard methodology. Each ligation was transformed into *E. coli* host 393 by electroporation utilizing the manufacturer's protocol. Clones were  
5 selected, plasmid DNA was isolated, and DNA sequencing was performed to verify the DNA sequence of either the muOPG met[27-189] or muOPG met[27-194] genes.

Expression of recombinant muOPG met[27-189] and muOPG met[27-194] following induction of 393 cells  
10 harboring recombinant pAMG21 plasmids was determined using methods described in Section C.

O. Human OPG met[22-185], met[22-189], met[22-194]

A DNA sequence coding for a N-terminal methionine and either amino acids 22 through 185, 22 through 189,  
15 or 22 through 194 of the human OPG polypeptide was placed under control of the lux PR promoter of prokaryotic expression vector pAMG21 as follows. The pair of synthetic oligonucleotides #1331-87 and #1331-88 (=huOPG-185 linker), #1331-89 and #1331-90 (=huOPG-  
20 189 linker), or #1331-91 & #1331-92 (=huOPG-194 linker) were phosphorylated individually and each allowed to form an oligo linker duplex pair using methods described in Section B. Purified plasmid DNA of pAMG21-huOPG-met[27-401] was restricted with KpnI and NdeI  
25 restriction endonucleases and the resulting DNA fragments were resolved on an agarose gel. The ~407 bp B fragment was isolated using standard recombinant DNA methodology. The phosphorylated oligo linker duplexes formed between either oligos #1331-87 and #1331-88  
30 (huOPG-185 linker), oligos #1331-89 and #1331-90 (huOPG-189 linker), or oligos #1331-91 and #1331-92 (huOPG-194 linker) [each linker contains NdeI and BamHI cohesive ends], and the isolated ~407 bp B fragment of plasmid pAMG21-huOPG-met[27-401] digested with KpnI and  
35 NdeI restriction endonucleases above, was directionally inserted between the KpnI and BamHI sites of plasmid



pAMG21-huOPG-met[22-401] using standard methodology. Each ligation was transformed into *E. coli* host 393 by electroporation utilizing the manufacturer's protocol. Clones were selected, plasmid DNA was isolated, and DNA  
 5 sequencing was performed to verify the DNA sequence of either the huOPG-met[22-185], huOPG-met[22-189], or huOPG-met[22-194] genes.

Expression of recombinant huOPG-met[22-185], huOPG-met[22-189] or huOPG-met[22-194] in transformed  
 10 393 cells harboring recombinant pAMG21 plasmids following induction was determined using methods described in Section C.

Oligo #1331-87:

5'-TAT GTT AAT GAG-3' (SEQ ID NO:85)

15 Oligo #1331-88:

5'-GAT CCT CAT TAA CA-3' (SEQ ID NO:86)

Oligo #1331-89:

5'-TAT GTT CCG GAA ACA GTT AAG-3' (SEQ ID NO:87)

Oligo #1331-90:

20 5'-GAT CCT TAA CTG TTT CCG GAA CA-3' (SEQ ID NO:88)

Oligo #1331-91:

5'-TAT GTT CCG GAA ACA GTG AAT CAA CTC AAA AAT AAG-3'  
 (SEQ ID NO:89)

Oligo #1331-92:

25 5'-GAT CCT TAT TTT TGA GTT GAT TCA CTG TTT CCG GAA CA-3'  
 (SEQ ID NO:90)

P. Human OPG met[27-185], met[27-189], met [27-194]

A DNA sequence coding for a N-terminal methionine and either amino acids 27 through 185, 27 through 189,  
 30 or 27 through 194 of the human OPG polypeptide was placed under control of the lux PR promoter of prokaryotic expression vector pAMG21 as follows. Phosphorylated oligo linkers "huOPG-185 linker", "huOPG-189 linker", or "huOPG-194 linker" (See Section  
 35 O) each containing NdeI and BamHI cohesive ends, and the isolated ~407 bp B fragment of plasmid pAMG21-



huOPG-met[27-401] digested with KpnI and NdeI restriction endonucleases (See Section O) were directionally inserted between the KpnI and BamHI sites of plasmid pAMG21-huOPG-met[27-401] (See Section J) using standard methodology. Each ligation was transformed into E. coli host 393 by electroporation utilizing the manufacturer's protocol. Clones were selected, plasmid DNA isolated, and DNA sequencing performed to verify the DNA sequence of either the huOPG-met[27-185], huOPG-met[27-189], or huOPG-met[27-194] genes.

Expression of recombinant huOPG-met[27-185], huOPG-met[27-189], and huOPG-met[27-194] from recombinant pAMG21 plasmids transformed into 393 cells was determined using methods described in Section C. O. Murine OPG met[27-401] (P33E, G36S, A45P)

A DNA sequence coding for an N-terminal methionine and amino acids 27 through 48 of human OPG followed by amino acid residues 49 through 401 of murine OPG was placed under control of the lux PR promoter of prokaryotic expression vector pAMG21 as follows. Purified plasmid DNA of pAMG21-huOPG-met[27-401] (See Section J) was cleaved with AatII and KpnI restriction endonucleases and a ~1075 bp B fragment isolated from an agarose gel using standard recombinant DNA methodology. Additionally, plasmid pAMG21-muOPG-met[22-401] DNA (See Section D) was digested with KpnI and BamHI restriction endonucleases and the ~1064 bp B fragment isolated as described above. The isolated ~1075 bp pAMG21-huOPG-met[27-401] restriction fragment containing AatII & KpnI cohesive ends (see above), the ~1064 bp pAMG21-muOPG-met[22-401] restriction fragment containing KpnI and BamHI sticky ends and a ~5043 bp restriction fragment containing AatII and BamHI cohesive ends and corresponding to the nucleic acid sequence of pAMG21 between AatII & BamHI were ligated



using standard recombinant DNA methodology. The ligation was transformed into E. coli host 393 by electroporation utilizing the manufacturer's protocol. Clones were selected, and the presence of the recombinant insert in the plasmid verified using standard DNA methodology. muOPG-27-401 (P33E, G36S, A45P) gene. Amino acid changes in muOPG from proline-33 to glutamic acid-33, glycine-36 to serine-36, and alanine-45 to proline-45, result from replacement of muOPG residues 27 through 48 with huOPG residues 27 through 48.

Expression of recombinant muOPG-met[27-401] (P33E, G36S, A45P) from transformed 393 cells harboring the recombinant pAMG21 plasmid was determined using methods described in Section C.

R. Murine OPG met-lys-(his)<sub>7</sub>-ala-ser-(asp)<sub>4</sub>-lys[22-401] (A45T)

A DNA sequence coding for an N-terminal His tag and enterokinase recognition sequence which is (NH<sub>2</sub> to COOH terminus): Met-Lys-His-His-His-His-His-His-Ala-Ser-Asp-Asp-Asp-Asp-Lys (=HEK), followed by amino acids 22 through 401 of the murine OPG polypeptide was placed under control of the lac repressor regulated Ps4 promoter as follows. pAMG22-His (See Section A) was digested with NheI and BamHI restriction endonucleases, and the large fragment (the A fragment) isolated from an agarose gel using standard recombinant DNA methodology. Oligonucleotides #1282-91 and #1282-92 were phosphorylated individually and allowed to form an oligo linker duplex using methods previously described (See Section B). The phosphorylated linker duplex formed between oligos #1282-91 and #1282-92 containing NheI and KpnI cohesive ends, the KpnI and BamHI digested and purified PCR product described (see Section D), and the A fragment of vector pAMG22-His



digested with NheI and BamHI were ligated using standard recombinant DNA methodology. The ligation was transformed into *E. coli* host GM120 by electroporation utilizing the manufacturer's protocol. Clones were  
 5 selected, plasmid DNA isolated and DNA sequencing performed to verify the DNA sequence of the muOPG-HEK[22-401] gene. DNA sequencing revealed a spurious mutation in the natural muOPG sequence that resulted in a single amino acid change of Alanine-45 of muOPG  
 10 polypeptide to a Threonine.

Expression of recombinant muOPG-HEK[22-401] (A45T) from GM120 cells harboring the recombinant pAMG21 plasmid was determined using methods similar to those described in Section C, except instead of addition of  
 15 the synthetic autoinducer, IPTG was added to 0.4 mM final to achieve induction.

Oligo #1282-91:

5'-CTA GCG ACG ACG ACG ACA AAG AAA CTC TGC CTC CAA AAT ACC TGC ATT  
 ACG ATC CGG AAA CTG GTC ATC AGC TGC TGT GTG ATA AAT GTG CTC CGG  
 20 GTA C-3' (SEQ ID NO:91)

Oligo #1282-92:

5'-CCG GAG CAC ATT TAT CAC ACA GCA GCT GAT GAC CAG TTT CCG GAT CGT  
 AAT GCA GGT ATT TTG GAG GCA GAG TTT CTT TGT CGT CGT CGT CG-3'  
 (SEQ ID NO:92)

25 S. Human OPG met-arg-gly-ser-(his)<sub>6</sub>[22-401]

Eight oligonucleotides (1338-09 to 1338-16 shown below) were designed to produce a 175 base fragment as overlapping, double stranded DNA. The oligos were annealed, ligated, and the 5' and 3' oligos were used  
 30 as PCR primers to produce large quantities of the 175 base fragment. The final PCR gene products were digested with restriction endonucleases ClaI and KpnI to yield a fragment which replaces the N-terminal 28 codons of human OPG. The ClaI and KpnI digested PCR  
 35 product was inserted into pAMG21-huOPG [27-401] which had also been cleaved with ClaI and KpnI. Ligated DNA



was transformed into competent host cells of *E. coli* strain 393. Clones were screened for the ability to produce the recombinant protein product and to possess the gene fusion having the correct nucleotide sequence.

5 Protein expression levels were determined from 50 ml shaker flask studies. Whole cell lysate and sonic pellet were analyzed for expression of the construct by Coomassie stained PAGE gels and Western analysis with murine anti-OPG antibody. Expression of huOPG Met-Arg-

10 Gly-Ser-(His)<sub>6</sub> [22-401] resulting in the formation of large inclusion bodies and the protein was localized to the insoluble (pellet) fraction.

1338-09:

ACA AAC ACA ATC GAT TTG ATA CTA GA (SEQ ID NO:93)

15 1338-10:

TTT GTT TTA ACT AAT TAA AGG AGG AAT AAA ATA TGA GAG GAT CGC ATC AC  
(SEQ ID NO:94)

1338-11:

20 CAT CAC CAT CAC GAA ACC TTC CCG CCG AAA TAC CTG CAC TAC GAC GAA GA  
(SEQ ID NO:95)

1338-12:

AAC CTC CCA CCA GCT GCT GTG CGA CAA ATG CCC GCC GGG TAC CCA AAC A  
(SEQ ID NO:96)

1338-13:

25 TGT TTG GGT ACC CGG CGG GCA TTT GT (SEQ ID NO:97)

1338-14:

CGC ACA GCA GCT GGT GGG AGG TTT CTT CGT CGT AGT GCA GGT ATT TCG GC  
(SEQ ID NO:98)

1338-15:

30 GGG AAG GTT TCG TGA TGG TGA TGG TGA TGC GAT CCT CTC ATA TTT TAT T  
(SEQ ID NO:99)

1338-16:

CCT CCT TTA ATT AGT TAA AAC AAA TCT AGT ATC AAA TCG ATT GTG TTT GT  
(SEQ ID NO:100)

35 T. Human OPG met-lys[22-401] and met(lys)<sub>3</sub>[22-401]

To construct the met-lys and met-(lys)<sub>3</sub> versions of human OPG[22-401], overlapping oligonucleotides were designed to add the appropriate number of lysine



residues. The two oligos for each construct were designed to overlap, allowing two rounds of PCR to produce the final product. The template for the first PCR reaction was a plasmid DNA preparation containing the human OPG 22-401 gene. The first PCR added the lysine residue(s). The second PCR used the product of the first round and added sequence back to the first restriction site, ClaI.

The final PCR gene products were digested with restriction endonucleases ClaI and KpnI, which replace the N-terminal 28 codons of hu OPG, and then ligated into plasmid pAMG21-hu OPG [27-401] which had been also digested with the two restriction endonucleases. Ligated DNA was transformed into competent host cells of *E. coli* strain 393. Clones were screened for the ability to produce the recombinant protein product and to possess the gene fusion having the correct nucleotide sequence. Protein expression levels were determined from 50 ml shaker flask studies. Whole cell lysate and sonic pellet were analyzed for expression of the construct by Coomassie stained PAGE gels and Western analysis with murine anti-OPG antibody. Neither construct had a detectable level of protein expression and inclusion bodies were not visible. The DNA sequences were confirmed by DNA sequencing. Oligonucleotide primers to prepare Met-Lys huOPG[22-401]:

1338-17:

ACA AAC ACA ATC GAT TTG ATA CTA GAT TTG TTT TAA CTA ATT AAA GGA  
GGA ATA AAA TG (SEQ ID NO:101)

1338-18:

CTA ATT AAA GGA GGA ATA AAA TGA AAG AAA CTT TTC CTC CAA AAT ATC  
(SEQ ID NO:102)

1338-20:

TGT TTG GGT ACC CGG CGG ACA TTT ATC ACA C (SEQ ID NO:103)



Oligonucleotide primers to prepare Met-(Lys)<sub>3</sub>-huOPG[22-401]:

1338-17:

ACA AAC ACA ATC GAT TTG ATA CTA GAT TTG TTT TAA CTA ATT AAA GGA  
5 GGA ATA AAA TG (SEQ ID NO:104)

1338-19:

CTA ATT AAA GGA GGA ATA AAA TGA AAA AAA AAG AAA CTT TTC CTC CAA  
AAT ATC (SEQ ID NO:105)

1338-20:

10 TGT TTG GGT ACC CGG CGG ACA TTT ATC ACA C (SEQ ID NO:106)  
U. Human and Murine OPG [22-401]/Fc Fusions

Four OPG-Fc fusions were constructed where the Fc region of human IgG1 was fused at the N-terminus of either human or murine Osteoprotegerin amino acids 22 to 401 (referred to as Fc/OPG [22-401]) or at the C-terminus (referred to as OPG[22-401]/Fc). Fc fusions were constructed using the fusion vector pFc-A3 described in Example 7.

All fusion genes were constructed using standard PCR technology. Template for PCR reactions were plasmid preparations containing the target genes. Overlapping oligos were designed to combine the C-terminal portion of one gene with the N terminal portion of the other gene. This process allows fusing the two genes together in the correct reading frame after the appropriate PCR reactions have been performed. Initially one "fusion" oligo for each gene was put into a PCR reaction with a universal primer for the vector carrying the target gene. The complimentary "fusion" oligo was used with a universal primer to PCR the other gene. At the end of this first PCR reaction, two separate products were obtained, with each individual gene having the fusion site present, creating enough overlap to drive the second round of PCR and create the desired fusion. In the second round of PCR, the first two PCR products were combined along with universal primers and via the



overlapping regions, the full length fusion DNA sequence was produced.

The final PCR gene products were digested with restriction endonucleases XbaI and BamHI, and then ligated into the vector pAMG21 having been also digested with the two restriction endonucleases. Ligated DNA was transformed into competent host cells of E. coli strain 393. Clones were screened for the ability to produce the recombinant protein product and to possess the gene fusion having the correct nucleotide sequence. Protein expression levels were determined from 50 ml shaker flask studies. Whole cell lysate, sonic pellet, and supernatant were analyzed for expression of the fusion by Coomassie stained PAGE gels and Western analysis with murine anti-OPG antibody.

Fc/huOPG [22-401]

Expression of the Fc/hu OPG [22-401] fusion peptide was detected on a Coomassie stained PAGE gel and on a Western blot. The cells have very large inclusion bodies, and the majority of the product is in the insoluble (pellet) fraction. The following primers were used to construct this OPG-Fc fusion:

1318-48:

CAG CCC GGG TAA AAT GGA AAC GTT TCC TCC AAA ATA TCT TCA TT  
(SEQ ID NO:107)

1318-49:

CGT TTC CAT TTT ACC CGG GCT GAG CGA GAG GCT CTT CTG CGT GT  
(SEQ ID NO:108)

Fc/muOPG [22-401]

Expression of the fusion peptide was detected on a Coomassie stained gel and on a Western blot. The cells have very large inclusion bodies, and the majority of the product is in the insoluble (pellet) fraction. The following primers were used to construct this OPG-Fc fusion:

1318-50:



CGC TCA GCC CGG GTA AAA TGG AAA CGT TGC CTC CAA AAT ACC TGC  
(SEQ ID NO:109)

1318-51:

CCA TTT TAC CCG GGC TGA GCG AGA GGC TCT TCT GCG TGT  
5 (SEQ ID NO:110)

muOPG [22-401]/Fc ;

Expression of the fusion peptide was detected on a  
Coomassie stained gel and on a Western blot. The amount  
of recombinant product was less than the OPG fusion  
10 proteins having the Fc region in the N terminal  
position. Obvious inclusion bodies were not detected.  
Most of the product appeared to be in the insoluble  
(pellet) fraction. The following primers were used to  
construct this OPG-Fc fusion:

15 1318-54:

GAA AAT AAG CTG CTT AGC TGC AGC TGA ACC AAA ATC (SEQ ID NO:111)

1318-55:

CAG CTG CAG CTA AGC AGC TTA TTT TCA CGG ATT G (SEQ ID NO:112)

huOPG [22-401]/Fc

20 Expression of the fusion peptide was not detected  
on a Coomassie stained gel, although a faint Western  
positive signal was present. Obvious inclusion bodies  
were not detected. The following primers were used to  
prepare this OPG-Fc fusion:

25 1318-52:

AAA AAT AAG CTG CTT AGC TGC AGC TGA ACC AAA ATC (SEQ ID NO:113)

1318-53:

CAG CTG CAG CTA AGC AGC TTA TTT TTA CTG ATT GG (SEQ ID NO:114)

V. Human OPG met[22-401]-Fc fusion (P25A)

30 This construct combines a proline to alanine amino  
acid change at position 25 (P25A) with the huOPG  
met[22-401]-Fc fusion. The plasmid was digested with  
restriction endonucleases ClaI and KpnI, which removes  
the N-terminal 28 codons of the gene, and the resulting  
35 small (less than 200 base pair) fragment was gel  
purified. This fragment containing the proline to



alanine change was then ligated into plasmid pAMG21-huOPG [22-401]-Fc fusion which had been digested with the two restriction endonucleases. The ligated DNA was transformed into competent host cells of E. coli strain 5 393. Clones were screened for the ability to produce the recombinant protein product and to possess the gene fusion having the correct nucleotide sequence. Protein expression levels were determined from 50 ml shaker flask studies. Whole cell lysate and sonic pellet were 10 analyzed for expression of the construct by Coomassie stained PAGE gels and Western analysis with murine anti-OPG antibody. The expression level of the fusion peptide was detected on a Coomassie stained PAGE gel and on a Western blot. The protein was in the insoluble 15 (pellet) fraction. The cells had large inclusion bodies.

W. Human OPG met[22-401] (P25A)

A DNA sequence coding for an N-terminal methionine and amino acids 22 through 401 of human OPG with the 20 proline at position 25 being substituted by alanine under control of the lux Pr promoter in prokaryotic expression vector pAMG21 was constructed as follows: Synthetic oligos # 1289-84 and 1289-85 were annealed to form an oligo linker duplex with XbaI and KpnI cohesive 25 ends. The synthetic linker duplex utilized optimal E. coli codons and encoded an N-terminal methionine. The linker also included an SpeI restriction site which was not present in the original sequence. The linker duplex was directionally inserted between the XbaI and KpnI 30 sites in pAMG21-huOPG-22-401 using standard methods. The ligation mixture was introduced into E. coli host GM221 by transformation. Clones were initially screened for production of the recombinant protein. Plasmid DNA was isolated from positive clones and DNA sequencing 35 was performed to verify the DNA sequence of the HuOPG-



Met[22-401](P25A) gene. The following oligonucleotides were used to generate the XbaI - KpnI linker:

Oligo #1289-84:

5'-CTA GAA GGA GGA ATA ACA TAT GGA AAC TTT TGC TCC AAA ATA TCT TCA  
5 TTA TGA TGA AGA AAC TAG TCA TCA GCT GCT GTG TGA TAA ATG TCC GCC  
GGG TAC -3' (SEQ ID NO:115)

Oligo #1289-85:

5'-CCG GCG GAC ATT TAT CAC ACA GCA GCT GAT GAC TAG TTT CTT CAT CAT  
AAT GAA GAT ATT TTG GAG CAA AAG TTT CCA TAT GTT ATT CCT CCT T-3'  
10 (SEQ ID NO:116)

X. Human OPG met[22-401] (P26A) and (P26D)

A DNA sequence coding for an N-terminal methionine and amino acids 22, through 401 of human OPG with the proline at position 26 being substituted by alanine  
15 under control of the lux Pr promoter in prokaryotic expression vector pAMG21 was constructed as follows: Synthetic oligos # 1289-86 and 1289-87 were annealed to form an oligo linker duplex with XbaI and SpeI cohesive ends. The synthetic linker duplex utilized optimal *E.*  
20 *coli* codons and encoded an N-terminal methionine. The linker duplex was directionally inserted between the XbaI and SpeI sites in pAMG21-huOPG[22-401](P25A) using standard methods. The ligation mixture was introduced into *E. coli* host GM221 by transformation. Clones were  
25 initially screened for production of the recombinant protein. Plasmid DNA was isolated from positive clones and DNA sequencing was performed to verify the DNA sequence of the huOPG-met[22-401](P26A) gene. One of the clones sequenced was found to have the proline at  
30 position 26 substituted by aspartic acid rather than alanine, and this clone was designated huOPG-met[22-401](P26D). The following oligonucleotides were used to generate the XbaI - SpeI linker:

Oligo #1289-86:

35 5' - CTA GAA GGA GGA ATA ACA TAT GGA AAC TTT TCC TGC TAA ATA TCT  
TCA TTA TGA TGA AGA AA - 3' (SEQ ID NO:117)



Oligo #1289-87:

5' - CTA GTT TCT TCA TCA TAA TGA AGA TAT TTA GCA GGA AAA GTT TCC  
ATA TGT TAT TCC TCC TT - 3' (SEQ ID NO:118)

Y. Human OPG met[22-194] (P25A)

- 5 A DNA sequence coding for an N-terminal methionine and amino acids 22 through 194 of human OPG with the proline at position 25 being substituted by alanine under control of the lux Pr promoter in prokaryotic expression vector pAMG21 was constructed as follows:
- 10 The plasmids pAMG21-huOPG[27-194] and pAMG21-huOPG[22-401] (P25A) were each digested with KpnI and BamHI endonucleases. The 450 bp fragment was isolated from pAMG21-huOPG[27-194] and the 6.1 kbp fragment was isolated from pAMG21-huOPG[22-401] (P25A). These
- 15 fragments were ligated together and introduced into E. coli host GM221 by transformation. Clones were initially screened for production of the recombinant protein. Plasmid DNA was isolated from positive clones and DNA sequencing was performed to verify the DNA
- 20 sequence of the huOPG-Met[22-194] (P25A) gene.

#### EXAMPLE 9

##### Association of OPG Monomers

- CHO cells engineered to overexpress muOPG [22-401] were used to generate conditioned media for the
- 25 analysis of secreted recombinant OPG using rabbit polyclonal anti-OPG antibodies. An aliquot of conditioned media was concentrated 20-fold, then analysed by reducing and non-reducing SDS-PAGE (Figure 15). Under reducing conditions, the protein
- 30 migrated as a Mr 50-55 kd polypeptide, as would be predicted if the mature product was glycosylated at one or more of its consensus N-linked glycosylation sites. Surprisingly, when the same samples were analysed by non-reducing SDS-PAGE, the majority of the protein
- 35 migrated as an approximately 100 kd polypeptide, twice the size of the reduced protein. In addition, there was



a smaller amount of the Mr 50-55 kd polypeptide. This pattern of migration on SDS-PAGE was consistent with the notion that the OPG product was forming dimers through oxidation of a free sulfhydryl group(s).

5       The predicted mature OPG polypeptide contains 23 cysteine residues, 18 of which are predicted to be involved in forming intrachain disulfide bridges which comprise the four cysteine-rich domains (Figure 12A). The five remaining C-terminal cysteine residues are not  
10 involved in secondary structure which can be predicted based upon homology with other TNFR family members. Overall there is a net uneven number of cysteine residues, and it is formally possible that at least one residue is free to form an intermolecular disulfide  
15 bond between two OPG monomers.

To help elucidate patterns of OPG kinesis and monomer association, a pulse-chase labelling study was performed. CHO cells expressing muOPG [22-401] were metabolically labelled as described above in serum-free  
20 medium containing <sup>35</sup>S methionine and cysteine for 30 min. After this period, the media was removed, and replaced with complete medium containing unlabelled methionine and cysteine at levels approximately 2,000-fold excess to the original concentration of  
25 radioactive amino acids. At 30 min, 1hr, 2 hr, 4 hr, 6 hr and 12 hr post addition, cultures were harvested by the removal of the conditioned media, and lysates of the conditioned media and adherent monolayers were prepared. The culture media and cell lysates were  
30 clarified as described above, and then immunoprecipitated using anti-OPG antibodies as described above. After the immunoprecipitates were washed, they were released by boiling in non-reducing SDS-PAGE buffer then split into two equal halves. To  
35 one half, the reducing agent  $\beta$ -mercaptoethanol was added



to 5% (v/v) final concentration, while the other half was maintained in non-reducing conditions. Both sets of immunoprecipitates were analysed by SDS-PAGE as described above, then processed for autoradiography and exposed to film. The results are shown in Figure 16. The samples analysed by reducing SDS-PAGE are depicted in the bottom two panels. After synthesis, the OPG polypeptide is rapidly processed to a slightly larger polypeptide, which probably represents modification by N-linked glycosylation. After approximately 1-2 hours, the level of OPG in the cell decreases dramatically, and concomitantly appears in the culture supernatant. This appears to be the result of the vectorial transport of OPG from the cell into the media over time, consistent with the notion that OPG is a naturally secreted protein. Analysis of the same immunoprecipitates under nonreducing conditions reveals the relationship between the formation of OPG dimers and secretion into the conditioned media (Figure 16, upper panels). In the first 30-60 minutes, OPG monomers are processed in the cell by apparent glycosylation, followed by dimer formation. Over time, the bulk of OPG monomers are driven into dimers, which subsequently disappear from the cell. Beginning about 60 minutes after synthesis, OPG dimers appear in the conditioned media, and accumulate over the duration of the experiment. Following this period, OPG dimers are formed, which are then secreted into the culture media. OPG monomers persist at a low level inside the cell over time, and small amounts also appear in the media. This does not appear to be the result of breakdown of covalent OPG dimers, but rather the production of sub-stoichiometric amounts of monomers in the cell and subsequent secretion.

Recombinantly produced OPG from transfected CHO cells appears to be predominantly a dimer. To determine



if dimerization is a natural process in OPG synthesis, we analysed the conditioned media of a cell line found to naturally express OPG. The CTLL-2 cell line, a murine cytotoxic T lymphocytic cell line (ATCC  
5 accession no. TIB-214), was found to express OPG mRNA in a screen of tissue and cell line RNA. The OPG transcript was found to be the same as the cloned and sequenced 2.5-3.0 kb RNA identified from kidney and found to encode a secreted molecule. Western blot  
10 analysis of conditioned media obtained from CTLL-2 cells shows that most, if not all, of the OPG secreted is a dimer (Figure 17). This suggests that OPG dimerization and secretion is not an artifact of overexpression in a cell line, but is likely to be the  
15 main form of the product as it is produced by expressing cells.

Normal and transgenic mouse tissues and serum were analysed to determine the nature of the OPG molecule expressed in OPG transgenic mice. Since the rat OPG  
20 cDNA was expressed under the control of a hepatocyte control element, extracts made from the parenchyma of control and transgenic mice under non-reducing conditions were analysed (Figure 18). In extract from transgenic, but not control mice, OPG dimers are  
25 readily detected, along with substoichiometric amounts of monomers. The OPG dimers and monomers appear identical to the recombinant murine protein expressed in the genetically engineered CHO cells. This strongly suggests that OPG dimers are indeed a natural form of  
30 the gene product, and are likely to be key active components. Serum samples obtained from control and transgenic mice were similarly analysed by western blot analysis. In control mice, the majority of OPG migrates as a dimer, while small amounts of monomer are also  
35 detected. In addition, significant amounts of a larger OPG related protein is detected, which migrates with a



relative molecular mass consistent with the predicted size of a covalently-linked trimer. Thus, recombinant OPG is expressed predominantly as a dimeric protein in OPG transgenic mice, and the dimer form may be the basis for the osteopetrotic phenotype in OPG mice. OPG recombinant protein may also exist in higher molecular weight "trimeric" forms.

To determine if the five C-terminal cysteine residues of OPG play a role in homodimerization, the murine OPG codons for cysteine residues 195 (C195), C202, C277, C319, and C400 were changed to serine using the QuickChange™ Site-Directed Mutagenesis Kit (Stratagene, San Diego, CA) as described above. The muOPG gene was subcloned between the Not I and Xba I sites of the pcDNA 3.1 (+) vector (Invitrogen, San Diego, CA). The resulting plasmid, pcDNA3.1-muOPG, and mutagenic primers were treated with Pfu polymerase in the presence of deoxynucleotides, then amplified in a thermocycler as described above. An aliquot of the reaction is then transfected into competent *E. coli* XL1-Blue by heatshock, then plated. Plasmid DNA from transformants was then sequenced to verify mutations.

The following primer pairs were used to change the codon for cysteine residue 195 to serine of the murine OPG gene, resulting in the production of a muOPG [22-401] C195S protein:

1389-19:

5' -CAC GCA AAA GTC GGG AAT AGA TGT CAC-3' (SEQ ID NO:150)

1406-38:

5' -GTG ACA TCT ATT CCC GAC TTT TGC GTG-3' (SEQ ID NO:151)

The following primer pairs were used to change the codon for cysteine residue 202 to serine of the murine OPG gene, resulting in the production of a muOPG [22-401] C202S protein:

1389-21:

5' -CAC CCT GTC GGA AGA GGC CTT CTT C-3' (SEQ ID NO:152)



1389-22:

5' -GAA GAA GGC CTC TTC CGA CAG GGT G-3' (SEQ ID NO:153)

The following primer pairs were used to change the codon for cysteine residue 277 to serine of the murine OPG gene, resulting in the production of a muOPG [22-401] C277S protein:

1389-23:

5' -TGA CCT CTC GGA AAG CAG CGT GCA-3' (SEQ ID NO:154)

1389-24:

10 5' -TGC ACG CTG CTT TCC GAG AGG TCA-3' (SEQ ID NO:155)

The following primer pairs were used to change the codon for cysteine residue 319 to serine of the murine OPG gene, resulting in the production of a muOPG [22-401] C319S protein:

15 1389-17:

5' -CCT CGA AAT CGA GCG AGC AGC TCC-3' (SEQ ID NO:156)

1389-18:

5' -CGA TTT CGA GGT CTT TCT CGT TCT C-3' (SEQ ID NO:157)

The following primer pairs were used to change the codon for cysteine residue 400 to serine of the murine OPG gene, resulting in the production of a muOPG [22-401] C400S protein:

1406-72:

25 5' -CCG TGA AAA TAA GCT CGT TAT AAC TAG GAA TGG-3'  
(SEQ ID NO:158)

1406-75:

5' -CCA TTC CTA GTT ATA ACG AGC TTA TTT TCA CGG-3'  
(SEQ ID NO:159)

Each resulting muOPG [22-401] plasmid containing the appropriate mutation was then transfected into human 293 cells, the mutant OPG-Fc fusion protein purified from conditioned media as described above. The biological activity of each protein was assessed the in vitro osteoclast forming assay described in example 11. Conditioned media from each transfectant was analysed



by non-reducing SDS-PAGE and western blotting with anti-OPG antibodies.

Mutation of any of the five C-terminal cysteine residues results in the production of predominantly  
5 (>90%) monomeric 55 kd OPG molecules. This strongly suggests that the C-terminal cysteine residues together play a role in OPG homodimerization.

C-terminal OPG deletion mutants were constructed to map the region(s) of the OPG C-terminal domain which  
10 are important for OPG homodimerization. These OPG mutants were constructed by PCR amplification using primers which introduce premature stop translation signals in the C-terminal region of murine OPG. The 5' oligo was designed to the MuOPG start codon (containing  
15 a HindIII restriction site) and the 3' oligonucleotides (containing a stop codon and XhoI site) were designed to truncate the C-terminal region of muOPG ending at either threonine residue 200 (CT 200), proline 212 (CT212), glutamic acid 293 (CT-293), or serine 355 (CT-  
20 355).

The following primers were used to construct muOPG [22-200]:

1091-39:

5' -CCT CTG AGC TCA AGC TTC CGA GGA CCA CAA TGA ACA AG-3'  
25 (SEQ ID NO:160)

1391-91:

5' -CCT CTC TCG AGT CAG GTG ACA TCT ATT CCA CAC TTT TGC GTG GC-3'  
(SEQ ID NO:161)

The following primers were used to construct muOPG  
30 [22-212]:

1091-39:

5' -CCT CTG AGC TCA AGC TTC CGA GGA CCA CAA TGA ACA AG-3'  
(SEQ ID NO:162)

1391-90:

35 5' -CCT CTC TCG AGT CAA GGA ACA GCA AAC CTG AAG AAG GC -3'  
(SEQ ID NO:163)



The following primers were used to construct muOPG [22-293]:

1091-39:

5' -CCT CTG AGC TCA AGC TTC CGA GGA CCA CAA TGA ACA AG-3'

5 (SEQ ID NO:164)

1391-89:

5' -CCT CTC TCG AGT CAC TCT GTG GTG AGG TTC GAG TGG CC-3'

(SEQ ID NO:165)

The following primers were used to construct muOPG [22-355]:

1091-39:

5' -CCT CTG AGC TCA AGC TTC CGA GGA CCA CAA TGA ACA AG-3'

(SEQ ID NO:166)

1391-88:

15 5' CCT CTC TCG AGT CAG GAT GTT TTC AAG TGC TTG AGG GC-3'

(SEQ ID NO:167)

Each resulting muOPG-CT plasmid containing the appropriate truncation was then transfected into human 293 cells, the mutant OPG-Fc fusion protein purified from conditioned media as described above. The biological activity of each protein was assessed the in vitro osteoclast forming assay described in example 11. The conditioned medias were also analysed by non-reducing SDS-PAGE and western blotting using anti-OPG antibodies.

Truncation of the C-terminal region of OPG effects the ability of OPG to form homodimers. CT 355 is predominantly monomeric, although some dimer is formed. CT 293 forms what appears to be equal molar amounts of monomer and dimer, and also high molecular weight aggregates. However, CT 212 and CT 200 are monomeric.

#### EXAMPLE 10

##### Purification of OPG

##### A. Purification of mammalian OPG-Fc Fusion Proteins

35 5 L of conditioned media from 293 cells expressing an OPG-Fc fusion protein were prepared as follows. A



frozen sample of cells was thawed into 10 ml of 293S media (DMEM-high glucose, 1x L-glutamine, 10% heat inactivated fetal bovine serum (FBS) and 100 ug/ml hygromycin) and fed with fresh media after one day.

5 After three days, cells were split into two T175 flasks at 1:10 and 1:20 dilutions. Two additional 1:10 splits were done to scale up to 200 T175 flasks. Cells were at 5 days post-thawing at this point. Cells were grown to near confluency (about three days) at which time serum-

10 containing media was aspirated, cells were washed one time with 25 ml PBS per flask and 25 ml of SF media (DMEM-high glucose, 1x L-glutamine) was added to each flask. Cells were maintained at 5% CO<sub>2</sub> for three days at which point the media was harvested, centrifuged,

15 and filtered through 0.45m cellulose nitrate filters (Corning).

OPG-Fc fusion proteins were purified using a Protein G Sepharose column (Pharmacia) equilibrated in PBS. The column size varied depending on volume of

20 starting media. Conditioned media prepared as described above was loaded onto the column, the column washed with PBS, and pure protein eluted using 100mM glycine pH 2.7. Fractions were collected into tubes containing 1M Tris pH 9.2 in order to neutralize as quickly as

25 possible. Protein containing fractions were pooled, concentrated in either an Amicon Centricon 10 or Centriprep 10 and diafiltered into PBS. The pure protein is stored at -80°C.

Murine [22-401]-Fc, Murine [22-180]-Fc, Murine [22-194]-Fc, human [22-401]-Fc and human [22-201]Fc

30 were purified by this procedure. Murine [22-185]-Fc is purified by this procedure.

#### B. Preparation of anti-OPG antibodies

Three New Zealand White rabbits (5-8 lbs initial

35 wt) were injected subcutaneously with muOPG[22-401]-Fc fusion protein. Each rabbit was immunized on day 1 with



50 µg of antigen emulsified in an equal volume of  
Freunds complete adjuvant. Further boosts (Days 14 and  
28) were performed by the same procedure with the  
substitution of Freunds incomplete adjuvant. Antibody  
5 titers were monitored by EIA. After the second boost,  
the antisera revealed high antibody titers and 25ml  
production bleeds were obtained from each animal. The  
sera was first passed over an affinity column to which  
murine OPG-Fc had been immobilized. The anti-OPG  
10 antibodies were eluted with Pierce Gentle Elution  
Buffer containing 1% glacial acetic acid. The eluted  
protein was then dialyzed into PBS and passed over a Fc  
column to remove any antibodies specific for the Fc  
portion of the OPG fusion protein. The run through  
15 fractions containing anti-OPG specific antibodies were  
dialyzed into PBS.

C. Purification of murine OPG[22-401]

Antibody Affinity Chromatography

Affinity purified anti-OPG antibodies were  
20 diafiltered into coupling buffer (0.1M sodium carbonate  
pH 8.3, 0.5M NaCl), and mixed with CNBr-activated  
sepharose beads (Pharmacia) for two hours at room  
temperature. The resin was then washed with coupling  
buffer extensively before blocking unoccupied sites  
25 with 1M ethanolamine (pH 8.0) for two hours at room  
temperature. The resin was then washed with low pH  
(0.1M sodium acetate pH 4.0, 0.5M NaCl) followed by a  
high pH wash (0.1M Tris-HCl pH 8.0, 0.5M NaCl). The  
last washes were repeated three times. The resin was  
30 finally equilibrated with PBS before packing into a  
column. Once packed, the resin was washed with PBS. A  
blank elution was performed with 0.1M glycine-HCl,  
pH 2.5), followed by re-equilibration with PBS.

Concentrated conditioned media from CHO cells  
35 expressing muOPG[22-410] was applied to the column at a



low flow rate. The column was washed with PBS until UV absorbance measured at 280nm returned to baseline. The protein was eluted from the column first with 0.1M glycine-HCl (pH 2.5), re-equilibrated with PBS, and  
5 eluted with a second buffer (0.1M CAPS, pH 10.5), 1M NaCl). The two elution pools were diafiltered separately into PBS and sterile filtered before freezing at -20°C.

#### Conventional Chromatography

10 CHO cell conditioned media was concentrated 23x in an Amicon spiral wound cartridge (S10Y10) and diafiltered into 20mM tris pH 8.0. The diafiltered media was then applied to a Q-sepharose HP (Pharmacia) column which had been equilibrated with 20mM tris pH  
15 8.0. The column was then washed until absorbance at 280 nm reached baseline. Protein was eluted with a 20 column volume gradient of 0-300 mM NaCl in tris pH 8.0. OPG was detected using a western blot of column fractions.

20 Fractions containing OPG were pooled and brought to a final concentration of 300 mM NaCl, 0.2 mM DTT. A NiNTA superose (Qiagen) column was equilibrated with 20mM tris pH 8.0, 300 mM NaCl, 0.2 mM DTT after which the pooled fractions were applied. The column was  
25 washed with equilibration buffer until baseline absorbance was reached. Proteins were eluted from the column with a 0-30mM Imidazole gradient in equilibration buffer. Remaining proteins were washed off the column with 1M Imidazole. Again a western blot  
30 was used to detect OPG containing fractions.

Pooled fractions from the NiNTA column were dialyzed into 10 mM potassium phosphate pH 7.0, 0.2mM DTT. The dialyzed pool was then applied to a ceramic hydroxyapatite column (Bio-Rad) which had been  
35 equilibrated in 10mM phosphate buffer. After column washing, the protein was eluted with a 10-100 mM



potassium phosphate gradient over 20 column volumes. This was then followed by a 20 column volume gradient of 100-400 mM phosphate.

OPG was detected by coomassie blue staining of SDS-polyacrylamide gels and by western blotting. Fractions were pooled and diafiltered onto PBS and frozen at -80°C. The purified protein runs as a monomer and will remain so after diafiltration into PBS. The monomer is stable when stored frozen or at pH 5 at 4°C. However if stored at 4°C in PBS, dimers and what appears to be trimers and tetramers will form after one week.

D. Purification of human OPG met[22-401] from E. coli

The bacterial cell paste was suspended into 10 mM EDTA to a concentration of 15% (w/v) using a low shear homogenizer at 5°C. The cells were then disrupted by two homogenizations at 15,000 psi each at 5°C. The resulting homogenate was centrifuged at 5,000 x g for one hour at 5°C. The centrifugal pellet was washed by low shear homogenization into water at the original homogenization volume followed by centrifugation as before. The washed pellet was then solubilized to 15% (w/v) by a solution of (final concentration) 6 M guanidine HCl, 10 mM dithiothreitol, 10 mM TrisHCl, pH 8.5 at ambient temperature for 30 minutes. This solution was diluted 30-fold into 2M urea containing 50 mM CAPS, pH 10.5, 1 mM reduced glutathione and then stirred for 72 hours at 5°C. The OPG was purified from this solution at 25°C by first adjustment to pH 4.5 with acetic acid and then chromatography over a column of SP-HP Sepharose resin equilibrated with 25 mM sodium acetate, pH 4.5. The column elution was carried out with a linear sodium chloride gradient from 50 mM to 550 mM in the same buffer using 20 column volumes at a flow rate of 0.1 column volumes/minute. The peak fractions containing only the desired OPG form were



pooled and stored at 5°C or buffer exchanged into phosphate buffered saline, concentrated by ultrafiltration, and then stored at 5°C. This material was analyzed by reverse phase HPLC, SDS-PAGE, limulus  
5 amebocyte lysate assay for the presence of endotoxin, and N-terminal sequencing. In addition, techniques such as mass spectrometry, pH/temperature stability, fluorescence, circular dichroism, differential scanning calorimetry, and protease profiling assays may also be  
10 used to examine the folded nature of the protein.

#### EXAMPLE 11

##### Biological Activity of Recombinant OPG

Based on histology and histomorphometry, it appeared that hepatic overexpression of OPG in  
15 transgenic mice markedly decreased the numbers of osteoclasts leading to a marked increase in bone tissue (see Example 4). To gain further insight into potential mechanism(s) underlying this in vivo effect, various forms of recombinant OPG have been tested in an in  
20 vitro culture model of osteoclast formation (osteoclast forming assay). This culture system was originally devised by Udagawa (Udagawa et al. Endocrinology 125, 1805-1813 (1989), Proc. Natl. Acad. Sci. USA 87, 7260-7264 (1990)) and employs a combination of bone marrow  
25 cells and cells from bone marrow stromal cell lines. A description of the modification of this culture system used for these studies has been previously published (Lacey et al. Endocrinology 136, 2367-2376 (1995)). In  
30 this method, bone marrow cells, flushed from the femurs and tibiae of mice, are cultured overnight in culture media (alpha MEM with 10% heat inactivated fetal bovine serum) supplemented with 500 U/ml CSF-1 (colony stimulating factor 1, also called M-CSF), a  
35 hematopoietic growth factor specific for cells of the monocyte/macrophage family lineage. Following this incubation, the non-adherent cells are collected,



subjected to gradient purification, and then cocultured with cells from the bone marrow cell line ST2 ( $1 \times 10^6$  non-adherent cells :  $1 \times 10^5$  ST2 cells/ ml media). The media is supplemented with dexamethasone (100 nM) and the biologically-active metabolite of vitamin D3 known as 1,25 dihydroxyvitamin D3 (1,25 (OH) $_2$  D3, 10 nM). To enhance osteoclast appearance, prostaglandin E2 (250 nM) is added to some cultures. The coculture period usually ranges from 8 - 10 days and the media, with all of the supplements freshly added, is renewed every 3-4 days. At various intervals, the cultures are assessed for the presence of tartrate acid phosphatase (TRAP) using either a histochemical stain (Sigma Kit # 387A, Sigma, St. Louis, MO) or TRAP solution assay. The TRAP histochemical method allows for the identification of osteoclasts phenotypically which are multinucleated ( $\geq 3$  nuclei) cells that are also TRAP+. The solution assay involves lysing the osteoclast-containing cultures in a citrate buffer (100 mM, pH 5.0) containing 0.1% Triton X-100. Tartrate resistant acid phosphatase activity is then measured based on the conversion of p-nitrophenylphosphate (20 mM) to p-nitrophenol in the presence of 80 mM sodium tartrate which occurs during a 3-5 minute incubation at RT. The reaction is terminated by the addition of NaOH to a final concentration of 0.5 M. The optical density at 405 nm is measured and the results are plotted.

Previous studies (Udagawa *et al.* *ibid*) using the osteoclast forming assay have demonstrated that these cells express receptors for  $^{125}\text{I}$ -calcitonin (autoradiography) and can make pits on bone surfaces, which when combined with TRAP positivity confirm that the multinucleated cells have an osteoclast phenotype. Additional evidence in support of the osteoclast phenotype of the multinucleated cells that arise in



vitro in the osteoclast forming assay are that the cells express  $\alpha v$  and  $\beta 3$  integrins by immunocytochemistry and calcitonin receptor and TRAP mRNA by in situ hybridization (ISH).

- 5        The huOPG [22-401]-Fc fusion was purified from CHO cell conditioned media and subsequently utilized in the osteoclast forming assay. At 100 ng/ml of huOPG [22-401]-Fc, osteoclast formation was virtually 100% inhibited (Figure 19A). The levels of TRAP measured in  
10 lysed cultures in microtitre plate wells were also inhibited in the presence of OPG with an  $ID_{50}$  of approximately 3 ng/ml (Figure 20). The level of TRAP activity in lysates appeared to correlate with the relative number of osteoclasts seen by TRAP  
15 cytochemistry (compare Figures 19A-19G and 20). Purified human IgG1 and TNF- $\alpha$  inhibitor were also tested in this model and were found to have no inhibitory or stimulatory effects suggesting that the inhibitory effects of the huOPG [22-401]-Fc were due to  
20 the OPG portion of the fusion protein. Additional forms of the human and murine molecules have been tested and the cumulative data are summarized in Table 3.



Table 3  
Effects of various OPG forms on in vitro  
osteoclast formation

5	<u>OPG Construct</u>	<u>Relative Bioactivity in vitro</u>
	muOPG [22-401]-Fc	+++
	muOPG [22-194]-Fc	+++
	muOPG [22-185]-Fc	++
10	muOPG [22-180]-Fc	-
	muOPG [22-401]	+++
	muOPG [22-401] C195	+++
	muOPG [22-401] C202	+
	muOPG [22-401] C277	-
15	muOPG [22-401] C319	+
	muOPG [22-401] C400	+
	muOPG [22-185]	-
	muOPG [22-194]	++
	muOPG [22-200]	++
20	muOPG [22-212]	-
	muOPG [22-293]	+++
	muOPG [22-355]	+++
	huOPG [22-401]-Fc	+++
25	huOPG [22-201]-Fc	+++
	huOPG [22-401]-Fc P26A	+++
	huOPG [22-401]-Fc Y28F	+++
	huOPG [22-401]	+++
	huOPG [27-401]-Fc	++
30	huOPG [29-401]-Fc	++
	huOPG [32-401]-Fc	+/-
	+++ , ED <sub>50</sub> = 0.4-2 ng/ml	
	++ , ED <sub>50</sub> = 2-10 ng/ml	
35	+ , ED <sub>50</sub> = 10-100 ng/ml	
	- , ED <sub>50</sub> > 100 ng/ml	



The cumulative data suggest that murine and human OPG amino acid sequences 22-401 are fully active in vitro, when either fused to the Fc domain, or unfused. They inhibit in a dose-dependent manner and possess  
5 half-maximal activities in the 2-10 ng/ml range. Truncation of the murine C-terminus at threonine residue 180 inactivates the molecule, whereas truncations at cysteine 185 and beyond have full activity. The cysteine residue located at position 185  
10 is predicted to form an SS3 bond in the domain 4 region of OPG. Removal of this residue in other TNFR-related proteins has previously been shown to abrogate biological activity (Yan et al. (1994), J. Biol. Chem. 266: 12099-104). Our finding that muOPG[22-180]-Fc is  
15 inactive while muOPG[22-185]-Fc is active is consistent with these findings. This suggests that amino acid residues 22-185 define a region for OPG activity.

These findings indicate that like transgenically-expressed OPG, recombinant OPG also  
20 suppressed osteoclast formation as tested in the osteoclast forming assay. Time course experiments examining the appearance of TRAP+ cells,  $\beta$ 3+ cells, F480+ cells in cultures continuously exposed to OPG demonstrate that OPG blocks the appearance TRAP+ and  
25  $\beta$ 3+ cells, but not F480+ cells. In contrast, TRAP+ and  $\beta$ 3+ cells begin to appear as early as day 4 following culture establishment in control cultures. Only F480+ cells can be found in OPG-treated cultures and they appear to be present at qualitatively the same numbers  
30 as the control cultures. Thus, the mechanism of OPG effects in vitro appears to involve a blockade in osteoclast differentiation at a step beyond the appearance of monocyte-macrophages but before the appearance of cells expressing either TRAP or  $\beta$ 3  
35 integrins. Collectively these findings indicate that



OPG does not interfere with the general growth and differentiation of monocyte-macrophage precursors from bone marrow, but rather suggests that OPG specifically blocks the selective differentiation of osteoclasts from monocyte-macrophage precursors.

To determine more specifically when in the osteoclast differentiation pathway that OPG was inhibitory, a variation of the in vitro culture method was employed. This variation, described in (Lacey *et al. supra*), employs bone marrow macrophages as osteoclast precursors. The osteoclast precursors are derived by taking the nonadherent bone marrow cells after an overnight incubation in CSF-1/M-CSF, and culturing the cells for an additional 4 days with 1,000 - 2,000 U/ml CSF-1. Following 4 days of culture, termed the growth phase, the non-adherent cells are removed. The adherent cells, which are bone marrow macrophages, can then be exposed for up to 2 days to various treatments in the presence of 1,000 - 2,000 U/ml CSF-1. This 2 day period is called the intermediate differentiation period. Thereafter, the cell layers are again rinsed and then ST-2 cells ( $1 \times 10^5$  cell/ml), dexamethasone (100 nM) and  $1,25(\text{OH})_2 \text{D}_3$  (10 nM) are added for the last 8 days for what is termed the terminal differentiation period. Test agents can be added during this terminal period as well. Acquisition of phenotypic markers of osteoclast differentiation are acquired during this terminal period (Lacey *et al. ibid*).

huOPG [22-401]-Fc (100 ng/ml) was tested for its effects on osteoclast formation in this model by adding it during either the intermediate, terminal or, alternatively, both differentiation periods. Both TRAP cytochemistry and solution assays were performed. The results of the solution assay are shown in Figure 21.



HuOPG [22-401]-Fc inhibited the appearance of TRAP activity when added to both the intermediate and terminal or only the terminal differentiation phases. When added to the intermediate phase and then removed  
5 from the cultures by rinsing, huOPG [22-401]-Fc did not block the appearance of TRAP activity in culture lysates. The cytochemistry results parallel the solution assay data. Collectively, these observations indicate that huOPG [22-401]-Fc only needs to be  
10 present during the terminal differentiation period for it to exert its all of its suppressive effects on osteoclast formation.

B. In vivo IL-1- $\alpha$  and IL-1- $\beta$  challenge experiments

IL-1 increases bone resorption both systemically  
15 and locally when injected subcutaneously over the calvaria of mice (Boyce et al. (1989), Endocrinology 125: 1142-50). The systemic effects can be assessed by the degree of hypercalcemia and the local effects histologically by assessing the relative magnitude of  
20 the osteoclast-mediated response. The aim of these experiments was to determine if recombinant muOPG [22-401]-Fc could modify the local and/or systemic actions of IL-1 when injected subcutaneously over the same region of the calvaria as IL-1.

25 IL-1  $\beta$  experiment

Male mice (ICR Swiss white) aged 4 weeks were divided into the following treatment groups (5 mice per group): Control group: IL-1 treated animals (mice received 1 injection/day of 2.5 ug of IL-1- $\beta$ ); Low dose  
30 muOPG [22-401]-Fc treated animals (mice received 3 injections/day of 1  $\mu$ g of muOPG [22-401]-Fc); Low dose muopg [22-401]-Fc and IL-1- $\beta$ ; High dose muOPG [22-401]-Fc treated animals (mice receive 3 injections/day of 10  $\mu$ g muOPG [22-401]-Fc); High dose muOPG [22-401]-Fc and



IL-1- $\beta$ . All mice received the same total number of injections of either active factor or vehicle (0.1% bovine serum albumin in phosphate buffered saline). All groups are sacrificed on the day after the last  
5 injection. The weights and blood ionized calcium levels are measured before the first injections, four hours after the second injection and 24 hours after the third IL-1 injection, just before the animals were sacrificed. After sacrifice the calvaria were removed  
10 and processed for paraffin sectioning.

IL-1  $\alpha$  experiment

Male mice (ICR Swiss white) aged 4 weeks were divided into the following treatment groups (5 mice per group): Control group; IL-1- $\alpha$  treated animals (mice  
15 received 1 injection/day of 5 ug of IL-1- $\alpha$ ); Low dose muOPG [22-401]-Fc treated animals (mice received 1 injection/day of 10  $\mu$ g of muOPG [22-401]-Fc; Low dose muopg [22-401]-Fc and IL-1- $\alpha$ , (dosing as above); High dose muopg [22-401]-Fc treated animals (mice received 3  
20 injections/day of 10  $\mu$ g muOPG [22-401]-Fc; High dose muOPG [22-401]-Fc and IL-1- $\alpha$ . All mice received the same number of injections/day of either active factor or vehicle. All groups were sacrificed on the day after the last injection. The blood ionized calcium levels  
25 were measured before the first injection, four hours after the second injection and 24 hours after the third IL-1 injection, just before the animals were sacrificed. The animal weights were measured before the first injection, four hours after the second injection  
30 and 24 hours after the third IL-1 injection, just before the animals were sacrificed. After sacrifice the calvaria were removed and processed for paraffin sectioning.



### Histological methods

Calvarial bone samples were fixed in zinc formalin, decalcified in formic acid, dehydrated through ethanol and mounted in paraffin. Sections (5µm  
5 thick) were cut through the calvaria adjacent to the lambdoid suture and stained with either hematoxylin and eosin or reacted for tartrate resistant acid phosphatase activity (Sigma Kit# 387A) and counterstained with hematoxylin. Bone resorption was  
10 assessed in the IL-1 α treated mice by histomorphometric methods using the Osteomeasure (Osteometrics, Atlanta, GA) by tracing histologic features onto a digitizer platen using a microscope-mounted camera lucida attachment. Osteoclast numbers,  
15 osteoclast lined surfaces, and eroded surfaces were determined in the marrow spaces of the calvarial bone. The injected and non-injected sides of the calvaria were measured separately.

### Results

20 IL-1 α and IL-1 β produced hypercalcemia at the doses used, particularly on the second day, presumably by the induction of increased bone resorption systemically. The hypercalcemic response was blocked by muOPG [22-401]-Fc in the IL-1 beta treated mice and  
25 significantly diminished in mice treated with IL-1-α, an effect most apparent on day 2 (Figure 22A-22B).

Histologic analysis of the calvariae of mice treated with IL-1-α and beta shows that IL-1 treatments alone produce a marked increase in the indices of bone  
30 resorption including: osteoclast number, osteoclast lined surface, and eroded surface (surfaces showing deep scalloping due to osteoclastic action (Figure 23B). In response to IL-1 α or IL-1 β, the increases in bone resorption were similar on the injected and non-



injected sides of the calvaria. Muopg [22-401]-Fc injections reduced bone resorption in both IL-1- $\alpha$  and beta treated mice and in mice receiving vehicle alone but this reduction was seen only on the muopg [22-401]-Fc injected sides of the calvariae.

The most likely explanation for these observations is that muOPG [22-401]-Fc inhibited bone resorption, a conclusion supported by the reduction of both the total osteoclast number and the percentage of available bone surface undergoing bone resorption, in the region of the calvaria adjacent to the muOPG [22-401]-Fc injection sites. The actions of muOPG [22-401]-Fc appeared to be most marked locally by histology, but the fact that muOPG [22-401]-Fc also blunted IL-1 induced hypercalcemia suggests that muOPG [22-401]-Fc has more subtle effects on bone resorption systemically.

#### C. Systemic Effects of muOPG [22-401]-Fc in Growing Mice

Male BDF1 mice aged 3-4 weeks, weight range 9.2-15.7g were divided into groups of ten mice per group. These mice were injected subcutaneously with saline or muOPG [22-401]-Fc 2.5mg/kg bid for 14 days (5mg/kg/day). The mice were radiographed before treatment, at day 7 and on day 14. The mice were sacrificed 24 hours after the final injection. The right femur was removed, fixed in zinc formalin, decalcified in formic acid and embedded in paraffin. Sections were cut through the mid region of the distal femoral metaphysis and the femoral shaft. Bone density, by histomorphometry, was determined in six adjacent regions extending from the metaphyseal limit of the growth plate, through the primary and secondary spongiosa and into the femoral diaphysis (shaft). Each region was 0.5 X 0.5 mm<sup>2</sup>.



#### Radiographic changes

After seven days of treatment there was evidence of a zone of increased bone density in the spongiosa associated with the growth plates in the OPG treated mice relative to that seen in the controls. The effects were particularly striking in the distal femoral and the proximal tibial metaphases (Figure 24A-24B). However bands of increased density were also apparent in the vertebral bodies, the iliac crest and the distal tibia. At 14 days, the regions of opacity had extended further into the femoral and tibial shafts though the intensity of the radio-opacity was diminished. Additionally, there were no differences in the length of the femurs at the completion of the experiment or in the change in length over the duration of the experiment implying that OPG does not alter bone growth.

#### Histological Changes

The distal femoral metaphysis showed increased bone density in a regions 1.1 to 2.65 mm in distance from the growth plate (Figures 25 and 26A-26B). This is a region where bone is rapidly removed by osteoclast-mediated bone resorption in mice. In these rapidly growing young mice, the increase in bone in this region observed with OPG treatment is consistent with an inhibition of bone resorption.

#### D. Effects of Osteoprotegerin on Bone Loss Induced by Ovariectomy in the Rat

Twelve week old female Fisher rats were ovariectomized (OVX) or sham operated and dual xray absorptiometry (DEXA) measurements made of the bone density in the distal femoral metaphysis. After 3 days recovery period, the animals received daily injections for 14 days as follows: Ten sham operated animals received vehicle (phosphate buffered saline); Ten OVX animals received vehicle (phosphate buffered saline);



Six OVX animals received OPG-Fc 5mg/kg SC; Six OVX animals received pamidronate (PAM) 5mg/kg SC; Six OVX animals received estrogen (ESTR) 40ug/kg SC. After 7 and 14 days treatment the animals had bone density measured by DEXA. Two days after the last injection the animals were killed and the right tibia and femur removed for histological evaluation.

The DEXA measurements of bone density showed a trend to reduction in the bone density following ovariectomy that was blocked by OPG-Fc. Its effects were similar to the known antiresorptive agents estrogen and pamidronate. (Figure 27). The histomorphometric analysis confirmed these observations with OPG-Fc treatment producing a bone density that was significantly higher in OVX rats than that seen in untreated OVX rats (Figure 28). These results confirm the activity of OPG in the bone loss associated with withdrawal of endogenous estrogen following ovariectomy.

#### In vivo Summary

The in vivo actions of recombinant OPG parallel the changes seen in OPG transgenic mice. The reduction in osteoclast number seen in the OPG transgenic is reproduced by injecting recombinant OPG locally over the calvaria in both normal mice and in mice treated with IL-1  $\alpha$  or IL-1  $\beta$ . The OPG transgenic mice develop an osteopetrotic phenotype with progressive filling of the marrow cavity with bone and unremodelled cartilage extending from the growth plates from day 1 onward after birth. In normal three week old (growing) mice, OPG treatments also led to retention of bone and unremodelled cartilage in regions of endochondral bone formation, an effect observed radiographically and confirmed histologically. Thus, recombinant OPG produces phenotypic changes in normal animals similar



to those seen in the transgenic animals and the changes are consistent with OPG-induced inhibition of bone resorption. Based on in vitro assays of osteoclast formation, a significant portion of this inhibition is due to impaired osteoclast formation. Consistent with this hypothesis, OPG blocks ovariectomy-induced osteoporosis in rat. Bone loss in this model is known to be mediated by activated osteoclasts, suggesting a role for OPG in treatment of primary osteoporosis.

10

#### EXAMPLE 12

##### Pegylation Derivatives of OPG

##### Preparation of N-terminal PEG-OPG conjugates by reductive alkylation

HuOPG met [22-194] P25A was buffer exchanged into 25-50 mM NaOAc, pH 4.5-4.8 and concentrated to 2-5 mg/ml. This solution was used to conduct OPG reductive alkylation with monofunctional PEG aldehydes at 5-7 °C. PEG monofunctional aldehydes, linear or branched, MW=1 to 57 kDa (available from Shearwater Polymers) were added to the OPG solution as solids in amounts constituting 2-4 moles of PEG aldehyde per mole of OPG. After dissolution of polymer into the protein solution, sodium cyanoborohydride was added to give a final concentration of 15 to 20 mM in the reaction mixture from 1-1.6 M freshly prepared stock solution in cold DI water. The progress of the reaction and the extent of OPG PEGylation was monitored by size exclusion HPLC on a G3000SWXL column (Toso Haas) eluting with 100 mM NaPO<sub>4</sub>, 0.5 M NaCl, 10% ethanol, pH 6.9. Typically the reaction was allowed to proceed for 16-18 hours, after which the reaction mixture was diluted 6-8 times and the pH lowered to 3.5-4. The reaction mixture was fractionated by ion exchange chromatography (HP SP HiLoad 16/10, Pharmacia) eluting with 20 mM NaOAc pH 4 with a linear gradient to 0.75M NaCl over 25 column



volumes at a flow rate of 30 cm/h. Fractions of mono-, di- or poly- PEGylated OPG were pooled and characterized by SEC HPLC and SDS-PAGE. By N-terminal sequencing, it was determined that the monoPEG-OPG conjugate, the major reaction product in most cases, was 98% N-terminally PEG-modified OPG.

This procedure was generally used to prepare the following N-terminal PEG-OPG conjugates (where OPG is HuOPG met [22-194] P25A: 5 kD monoPEG, 10 kD mono branched PEG, 12 kD monoPEG, 20 kD monoPEG, 20 kD mono branched PEG, 25 kD monoPEG, 31 kD monoPEG, 57 kD monoPEG, 12 kD diPEG, 25 kD diPEG, 31 kD diPEG, 57 kD diPEG, 25 kD triPEG.

Preparation of PEG-OPG conjugates by acylation

HuOPG met [22-194] P25A was buffer exchanged into 50 mM BICINE buffer, pH 8 and concentrated to 2-3 mg/ml. This solution was used to conduct OPG acylation with monofunctional PEG N-hydroxysuccinimidyl esters at room temperature. PEG N-hydroxysuccinimidyl esters, linear or branched, MW=1 to 57 kDa (available from Shearwater Polymers) were added to the OPG solution as solids in amounts constituting 4-8 moles of PEG N-hydroxysuccinimidyl ester per mole of OPG. The progress of the reaction and the extent of OPG PEGylation was monitored by size exclusion HPLC on a G3000SWXL column (Toso Haas) eluting with 100 mM NaPO<sub>4</sub>, 0.5 M NaCl, 10% ethanol, pH 6.9. Typically the reaction was allowed to proceed for 1 hour, after which the reaction mixture was diluted 6-8 times and the pH lowered to 3.5-4. The reaction mixture was fractionated by ion exchange chromatography (HP SP HiLoad 16/10, Pharmacia) eluting with 20 mM NaOAc pH 4 with a linear gradient to 0.75M NaCl over 25 column volumes at a flow rate of 30 cm/h. Fractions of mono-, di- or poly- PEGylated OPG were pooled and characterized by SEC HPLC and SDS-PAGE.



This procedure was generally used to prepare the following PEG-OPG conjugates: 5 kD polyPEG, 20 kD polyPEG, 40 kD poly branched PEG, 50 kD poly PEG.

Preparation of dimeric PEG-OPG

- 5        HuOPG met [22-194] P25A is prepared for thiolation at 1-3 mg/ml in a phosphate buffer at near neutral pH. S-acetyl mecaptosuccinic anhydride (AMSA) is added in a 3-7 fold molar excess while maintaining pH at 7.0 and the rxn stirred at 4°C for 2 hrs. The monothiolated-OPG
- 10    is separated from unmodified and polythiolated OPG by ion exchange chromatography and the protected thiol deprotected by treatment with hydroxylamine. After deprotection, the hydroxylamine is removed by gel filtration and the resultant monothiolated-OPG is
- 15    subjected to a variety of thiol specific crosslinking chemistries. To generate a disulfide bonded dimer, the thiolated OPG at >1mg/ml is allowed to undergo air oxidation by dialysis in slightly basic phosphate buffer. The covalent thioether OPG dimer was prepared
- 20    by reacting the bis-maleimide crosslinker, N,N-bis(3-maleimido propionyl)-2-hydroxy 1,3 propane with the thiolated OPG at >1mg/ml at a 0.6x molar ratio of crosslinker:OPG in phosphate buffer at pH 6.5. Similarly, the PEG dumbbells are produced by reaction
- 25    of substoichiometric amounts of bis-maleimide PEG crosslinkers with thiolated OPG at >1mg/ml in phosphate buffer at pH 6.5. Any of the above dimeric conjugates may be further purified using either ion exchange or size exclusion chromatographies.
- 30        Dimeric PEG-OPG conjugates (where OPG is HuOPG met [22-194] P25A prepared using the above procedures include disulfide-bonded OPG dimer, covalent thioether OPG dimer with an aliphatic amine type crosslinker, 3.4 kD and 8kD PEG dumbbells and monobells.



PEG-OPG conjugates were tested for activity in vitro using the osteoclast maturation assay described in Example 11A and for activity in vivo by measuring increased bone density after injection into mice as described in Example 11C. The in vivo activity is shown below in Table 2.

Table 2

In vivo biological activity of Pegylated OPG

<u>OPG Construct</u>	<u>Increase in Tibial Bone Density</u>
muOPG met [22-194]	-
muOPG met [22-194] 5k PEG	+
muOPG met [22-194] 20k PEG	+
huOPG met [22-194] P25A	-
huOPG met [22-194] P25A 5k PEG	+
huOPG met [22-194] P25A 20k PEG	+
huOPG met [22-194] P25A 31k PEG	+
huOPG met [22-194] P25A 57k PEG	+
huOPG met [22-194] P25A 12k PEG	+
huOPG met [22-194] P25A 20k Branched PEG	+
huOPG met [22-194] P25A 8k PEG dimer	+
<u>huOPG met [22-194] P25A disulfide crosslink</u>	<u>+</u>

EXAMPLE 13

Effects of OPG-Fc during the course of Adjuvant  
Arthritis in Lewis rats

The aim of these studies is to investigate whether CHO produced OPG-Fc protects against adjuvant arthritis-associated bone mineral density loss in male Lewis rats.

Animals

Male Lewis rats (Charles River, Wilmington MA) 8-9 weeks of age (n = 6) at the time of mycobacteria in oil injection, were used. Two rats were housed per cage in an air conditioned environment (room temperature  $23 \pm 2$



C, relative humidity  $50 \pm 20\%$ ) that illuminated from 6:30 am to 6:30 p.m. Animals were fed a commercial rodent chow (#8640, Tek Lab, Madison WI); calcium and phosphorus contents were 1.2% and 1.0%, respectively.

- 5 All animals were sacrificed by carbon dioxide inhalation.

#### Induction and Measurement of Adjuvant Arthritis

- Adjuvant arthritis (AdA) was induced by a single injection of a suspension of Mycobacterium tuberculosis (Difco Laboratories, Detroit MI) in paraffin oil (Crescent Chemical Co., Hauppauge, NY). Mycobacteria were grounded in a mortar to fine powder and suspended in paraffin oil (10 mg/ml). The suspension was dispersed evenly just before injection of 0.05ml at the base of tail. Severity of inflammation was monitored by measuring the volume of hindpaws using volume displacement technique. The extent of inflammation was calculated as increase in paw volume compared to Day 0. In addition, body weight was measured daily.

#### 20 OPG treatment and DEXA bone mass measurement

- Male Lewis (normal and adjuvant-induced) rats received varying doses of OPG-Fc (22-194) by subcutaneous daily injection (See graphs below for dosing) from day 9 to day 15. At the end of the experiment (day 16) bone mass measurement (DexaScans) of the tibiotarsal region was performed with a Hologic QDR 4500 dual-energy x-ray absorptiometer.

#### Statistical Analysis

- All results were expressed as the mean  $\pm$  standard deviation of the mean. The p value of 0.05 was used in the calculation to determine whether there were any significant differences between any two groups. Statistical significance of difference was assessed by analysis of variance based on a Mann Whitney U test using Statsoft software (Statsoft, Tulsa, OK).



## Results

### OPG-Fc inhibits loss of Bone Mineral Density in adjuvant arthritis

To study the effects of OPG-Fc on BMD in adjuvant arthritis, paws from two experiments were analyzed by DEXA. The results of BMD measurements on the tibiotarsal region are shown in Figures 2 and 4. Bone protective effects were observed in rats with adjuvant-arthritis treated with OPG-Fc via subcutaneous daily injection (from day 9 to day 15 after mycobacteria injection). Treatment with OPG-Fc at 4, 1, 0.25, 0.06, .016, and 0.004 mg/kg showed 100%, 100%, 100%, 86%, 22, and 22% inhibition of bone mineral density loss respectively. Treatment of the intermediate and high doses of OPG-Fc (4 - 0.06 mg/kg) showed a statistically significant difference in BMD when compared to the OPG placebo treated control group ( $P < 0.05$ ).

However, treatment with OPG-Fc (at all doses) had no statistically significant effect on the severity of inflammation (Figure 1 and 3, AUC) or loss of body weight (data on file).

### Conclusion

In conclusion, the results demonstrate that OPG-Fc have great efficacy in preventing bone density loss in the tibiotarsal region in arthritic rats. The inhibitory effects of OPG-Fc against bone changes occurred without any anti-inflammatory actions.

### EXAMPLE 14

#### Combination treatment with OPG-Fc and STNF-RI on

#### Adjuvant Arthritis in Male Lewis Rats

Male Lewis rats were injected with 0.5 mg heat-killed Mycobacterium tuberculosis H37Ra in mineral oil at the base of the tail. Rats were monitored for paw swelling and weight loss. Arthritis (paw swelling) developed after about 10 days. Paw swelling was calculated daily relative to paw volume on day 9



(beginning of treatment) and the area under the curve (AUC) from day 9 to 15 is given in the graph (Figure 31A). On day 16 at the end of the experiment DexaScans of the rats were taken and the calcaneus was evaluated for loss of bone mineral density (BMD) as shown in Figure 31B.

\* \* \*

While the invention has been described in what is considered to be its preferred embodiments, it is not to be limited to the disclosed embodiments, but on the contrary, is intended to cover various modifications and equivalents included within the spirit and scope of the appended claims, which scope is to be accorded the broadest interpretation so as to encompass all such modifications and equivalents.



Claims

What is claimed is:

1. A method for treating conditions leading to bone loss, which comprises administering a therapeutically effective amount of a purified and isolated OPG protein in conjunction with substances selected from the group consisting of TNF- $\alpha$  inhibitors; serine protease inhibitors; IL-1 inhibitors; IL-6 inhibitors; IL-8 inhibitors; IL-18 inhibitors; ICE modulators; FGF-1 to FGF-10; FGF modulators; PAF antagonists; MMP modulators; NOS modulators; modulators of glucocorticoid receptor; modulators of glutamate receptor; modulators of LPS levels; and noradrenaline and modulators and mimetics thereof.
2. The method of Claim 1, wherein the OPG protein is OPG-Fc.
3. The method of claim 1, wherein an IL-1 inhibitor and the OPG protein are administered.
4. The method of claim 3, wherein the IL-1 inhibitor comprises an IL-1ra polypeptide.
5. The method of Claim 4, wherein the OPG protein comprises an Fc region.
6. The method of claim 1, wherein a TNF- $\alpha$  inhibitor and the OPG protein are administered.
7. The method of claim 6, wherein the TNF- $\alpha$  inhibitor comprises sTNFR-I, sTNFR-II, or a fragment of sTNF-RI or sTNF-RII linked to an Fc region.
8. The method of claim 6, wherein the TNF- $\alpha$  inhibitor comprises 30 kD PEG sTNFR-I.
9. The method of claim 6, wherein the TNF- $\alpha$  inhibitor comprises a 2.6 kD sTNF-RI fragment.
10. The method of claim 9, wherein the sTNF-RI fragment comprises 30 kD PEG.



11. The method of claim 6, wherein the TNF- $\alpha$  inhibitor comprises sTNF-RII linked to an Fc region.
12. The method of claim 6, wherein the TNF- $\alpha$  inhibitor is etanercept.
13. The method of Claim 10, wherein the OPG protein is OPG-Fc.
14. The method of claim 1, wherein a serine protease inhibitor and the OPG protein are administered.
15. The method of claim 14, wherein the serine protease inhibitor comprises a SLPI polypeptide.
16. The method of Claim 14, wherein the OPG protein is OPG-Fc.
17. The method of claim 1, wherein an IL-1 inhibitor, a TNF- $\alpha$  inhibitor, and the OPG protein are administered.
18. The method of claim 17, wherein the IL-1 inhibitor comprises an IL-1ra polypeptide.
19. The method of claim 17, wherein the TNF- $\alpha$  inhibitor comprises sTNFR-I, sTNFR-II, sTNFR fragments or sTNFR-Fc.
20. The method of claim 17, wherein the TNF- $\alpha$  inhibitor comprises 30 kD PEG-sTNFR-I.
21. The method of claim 17, wherein the sTNF-RI fragment is a 2.6 kD fragment.
22. The method of claim 21, wherein the sTNF-RI fragment comprises 30 kD PEG.
23. The method of claim 17, wherein the TNF- $\alpha$  inhibitor comprises sTNFR-II linked to an Fc region.
24. The method of claim 17, wherein the TNF- $\alpha$  inhibitor is etanercept.
25. The method of Claim 17, wherein the OPG protein is OPG-Fc.



26. The method of Claim 1, wherein an IL-1 inhibitor, a serine protease inhibitor, and the OPG protein are administered.
27. The method of claim 26, wherein the IL-1 inhibitor comprises an IL-1ra polypeptide.
28. The method of claim 26, wherein the serine protease inhibitor comprises a SLPI polypeptide.
29. The method of Claim 26, wherein the OPG protein is OPG-Fc.
30. The method of claim 1, wherein a serine protease inhibitor, a TNF- $\alpha$  inhibitor, and the OPG protein are administered.
31. The method of claim 30, wherein the serine protease inhibitor comprises a SLPI polypeptide.
32. The method of claim 17, wherein the TNF- $\alpha$  inhibitor comprises sTNFR-I, sTNFR-II, sTNFR fragments or sTNFR-Fc.
33. The method of claim 30, wherein the TNF- $\alpha$  inhibitor comprises 30 kD PEG sTNFR-I.
34. The method of claim 30, wherein the TNF- $\alpha$  inhibitor comprises sTNFR-II linked to an Fc region.
35. The method of claim 30, wherein the TNF- $\alpha$  inhibitor is etanercept.
36. The method of claim 30, wherein the TNF- $\alpha$  inhibitor comprises a 2.6 kD sTNF-RI fragment.
37. The method of claim 36, wherein the sTNF-RI fragment comprises 30 kD PEG.
38. The method of Claim 30, wherein the OPG protein is OPG-Fc.
39. The method of any of claims 17 to 38, wherein the condition treated is rheumatoid arthritis.
40. The method of any of claims 17 to 38, wherein the condition treated is multiple sclerosis.



41. The method of any of claims 17 to 38, wherein the condition treated is osteoporosis.
42. The method of any of claims 17 to 38, wherein the condition treated is osteomyelitis.
43. A method of treating an IL-1 mediated disease, which comprises administering therapeutically effective amounts of an IL-1 inhibitor and a serine protease inhibitor.
44. The method of claim 43, wherein the IL-1 inhibitor comprises an IL-1ra polypeptide.
45. The method of claim 43, wherein the serine protease inhibitor comprises a SLPI polypeptide.
46. The method of claim 43, wherein the IL-1 mediated disease is asthma.
47. The method of claim 43, wherein the IL-1 mediated disease is rheumatoid arthritis.
48. The method of claim 46, wherein the therapeutically effective amounts are delivered by pulmonary administration.
49. A method of treating TNF-mediated disease, which comprises administering therapeutically effective amounts of a TNF- $\alpha$  inhibitor and a serine protease inhibitor.
50. The method of claim 49, wherein the TNF- $\alpha$  inhibitor comprises sTNFR-I, sTNFR-II, sTNFR fragments or sTNFR-Fc.
51. The method of claim 49, wherein the TNF- $\alpha$  inhibitor comprises 30 kD PEG sTNFR-I.
52. The method of claim 49, wherein the TNF- $\alpha$  inhibitor comprises a 2.6 kD sTNF-RI fragment.
53. The method of claim 52, wherein the sTNF-RI fragment comprises 30 kD PEG.



54. The method of claim 49, wherein the TNF- $\alpha$  inhibitor comprises sTNFR-II linked to an Fc region.
55. The method of claim 49, wherein the TNF- $\alpha$  inhibitor is etanercept.
56. The method of claim 49, wherein the serine protease inhibitor comprises a SLPI polypeptide.
57. The method of claim 49, wherein the TNF-mediated disease is rheumatoid arthritis.
58. A method of treating inflammation, which comprises administering an IL-18 inhibitor, a TNF- $\alpha$  inhibitor, and an IL-1 inhibitor.
59. A method of treating rheumatoid arthritis, which comprises administering an IL-18 inhibitor, a TNF- $\alpha$  inhibitor, and an IL-1 inhibitor.
60. A method of treating SLE, which comprises administering an IL-18 inhibitor, a TNF- $\alpha$  inhibitor, and an IL-1 inhibitor.
61. A method of treating GvHD, which comprises administering an IL-18 inhibitor, a TNF- $\alpha$  inhibitor, and an IL-1 inhibitor.



FIG. 1A

	148	178	208	238	268	298
FRI-1	ALLVFLDIIEWTTQETFPKYLHYDPETGRQLLCDKCAPGTYLKQHC.TVRRKTLCTVRRKTLCPD					
SW:TNR2_HUMAN	30	40	50	60	70	80
	HALPAQVAFTPYAPEPGSTCRLLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCED					
	328					
FRI-1	YSYTDSWHTS					
	:  : :					
SW:TNR2_HUMAN	90	100	110	120	130	140
	STYTQLWNWVPECLSCGSRSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPL					

FIG. 1B

FRI-1	69	YLHYDPETGRQLLCDKCAPGTYLKQHC.TVRRKTLCTV.PCPDY.SYTD
TNFR profile	6	YHYDQNGRMCEECHMCQPGHFLVKHCKQPKRDTVCHKPCPEGVITYDDW
FRI-1	116 H	
TNFR profile	56 H	
		Z Score = 8.29



FIG. 1C

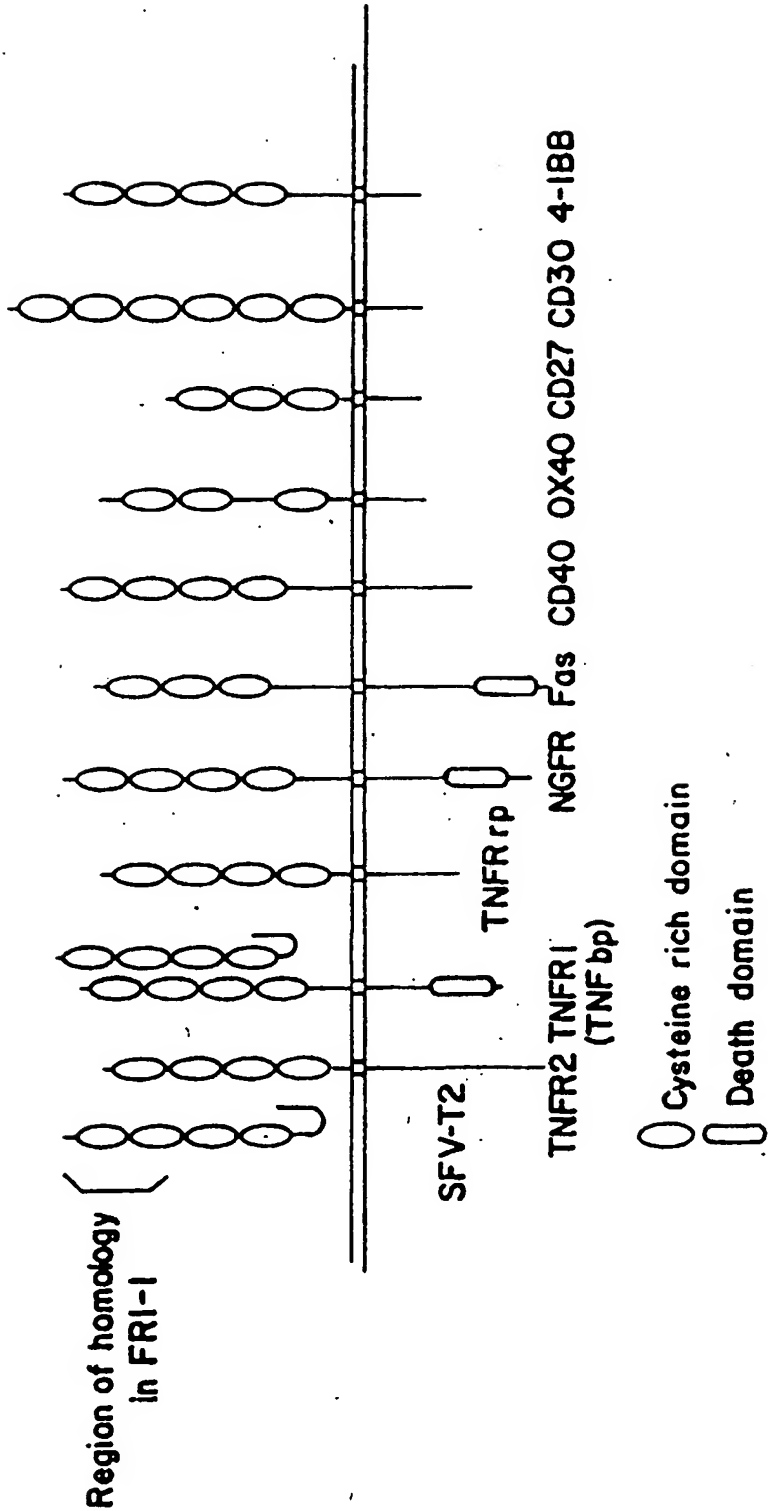




FIG.2A

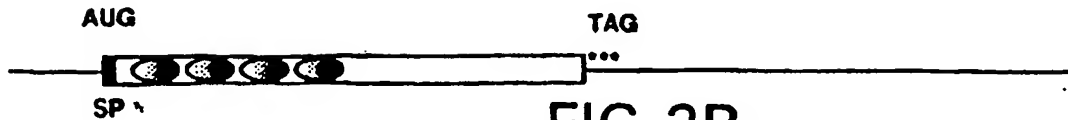


FIG.2B

10 30 50  
 ATCAAAGGCAGGGCATACTTCCTGTTGCCAGACCTTATATAAAACGTCATGTTTCGCCTG  
 70 90 110  
 GGCAGCAGAGAAGCACCTAGCACTGGCCAGCGGCTGCCGCCTGAGGTTCCAGAGGACC  
 130 150 170  
 ACAATGAACAAGTGGCTGTGCTGTGCACTCCTGGTGTCTTGGACATCATTGAATGGACA  
 M N K W L C C A L L V F L D I I E W T  
 190 210 230  
 ACCCAGGAAACCTTTCTCTCCAAATACCTTGCAATTATGACCCAGAAACCGACGTCAGCTC  
 T Q E T P P P K Y L H Y D P E T G R Q L  
 250 270 290  
 TTGTGTGACAAATGTGCTCCTGGCACCTACCTAAAAACAGCACTGCACAGTCAGGAGGAAG  
 L C D K C A P G T Y L K Q H C T V R R K  
 310 330 350  
 ACACTGTGTGTCCCTTGCCCTGACTACTCTTATACAGACAGCTGGCACACGAGTGATGAA  
 T L C V P C P D Y S Y T D S W H T S D E  
 370 390 410  
 TGCCTGTACTGCAGCCCCGTGTGCAAGGAAGTGCAGACCGTGAAACAGGAGTGCAACCGC  
 C V Y C S P V C K E L Q T V K Q E C M R  
 430 450 470  
 ACCCACAACCGAGTGTGCGAATGTGAGGAAGGGCGCTACCTGGAGCTCGAATTCTGCTTG  
 T H N R V C E C E E G R Y L E L E F C L  
 490 510 530  
 AAGCACCGGAGCTGTCCCCCAGGCTTGGGTGTGCTGCAGGCTGGGACCCAGAGCGAAAC  
 K H R S C P P G L G V L Q A G T P E R N  
 550 570 590  
 ACGGTTTGCAAAAGATGTCCGGATGGGTTCTTCTCAGGTGAGACGTCATCGAAAGCACCC  
 T V C K R C P D G P P S G E T S S K A P  
 610 630 650  
 TGTAGGAAACACACCAACTGCAGCTCACTTGGCCTCCTGCTAATTCAGAAAGGAAATGCA  
 C R K H T M C S S L G L L L I Q K G N A  
 670 690 710  
 ACACATGACAATGTATGTTCCGGAAACAGAGAAGCAACTCAAAATTGTGGAATAGATGTC  
 T H D N V C S G N R E A T Q N C G I D V  
 730 750 770  
 ACCCTGTGCGAAGAGGCATTCTTCAGGTTTGCTGTGCCTACCAAGATTATACCGAATTGG  
 T L C E E A P P R P A V P T K I I P N W  
 790 810 830  
 CTGAGTGTCTGGTGGACAGTTTGCCTGGGACCAAAGTGAATGCAGAGAGTGTAGAGAGG  
 L S V L V D S L P G T K V N A E S V E R  
 850 870 890  
 ATAAAACGGAGACACAGCTCGCAAGAGCAAACCTTCCAGCTACTTAAAGCTGTGGAAGCAT  
 I K R R H S S Q E Q T F Q L L K L W K H  
 910 930 950  
 CAAAACAGAGACCAGGAAATGGTGAAGAAGATCATCCAAGACATTGACCTCTGTGAAAGC  
 Q N R D Q E M V K K I I Q D I D L C E S  
 970 990 1010  
 AGTGTGCAACGGCATATCGGCCACGCGAACTCACCACAGAGCAGCTCCGCATCTTGATG  
 S V Q R H I G H A N L T T E Q L R I L M



## FIG.2C

1030 1050 1070  
GAGAGCTTGCCTGGGAAGAAGATCAGCCCAGACGAGATTGAGAGAACGAGAAAGACCTGC  
E S L P G K K I S P D E I E R T R K T C  
1090 1110 1130  
AAACCCAGCGAGCAGCTCCTGAAGCTACTGAGCTTGTGGAGGATCAAAAATGGAGACCAA  
K P S E Q L L K L L S L W R I K N G D Q  
1150 1170 1190  
GACACCTTGAAGGGCCTGATGTACGCACTCAAGCACTTGAAAGCATACCACTTTCCCAA  
D T L K G L M Y A L K H L K A Y H F P K  
1210 1230 1250  
ACCGTCACCCACAGTCTGAGGAAGACCATCAGGTTCTTGCACAGCTTCACCATGTACCGA  
T V T H S L R K T I R F L H S F T M Y R  
1270 1290 1310  
TTGTATCAGAACTCTTTCTAGAAATGATAGGAATCAGGTTCAATCAGTGAAGATAAGC  
L Y Q K L F L E M I G N Q V Q S V K I S  
1330 1350 1370  
TGCTTATAGTTAGGAATGGTCACTGGGCTGTTTCTTCAGGATGGGCCAACACTGATGGAG  
C L  
1390 1410 1430  
CAGATGGCTGCTTCTCCGGCTCTTGAAATGGCAGTTGATTCCTTTCTCATCAGTTGGTGG  
1450 1470 1490  
GAATGAAGATCCTCCAGCCCAACACACACACTGGGGAGTCTGAGTCAGGAGAGTGAGGCA  
1510 1530 1550  
GGCTATTTGATAATTGTGCAAAGCTGCCAGGTGTACACCTAGAAAGTCAAGCACCCCTGAG  
1570 1590 1610  
AAAGAGGATATTTTTATAACCTCAAACATAGGCCCTTTCCTTCCTCTCCTTATGGATGAG  
1630 1650 1670  
TACTCAGAAGGCTTCTACTATCTTCTGTGTCATCCCTAGATGAAGGCCTCTTTTATTTAT  
1690 1710 1730  
TTTTTTATTCTTTTTTTCGGAGCTGGGGACCGAACCCAGGGCCTTGCGCTTGCGAGGCAA  
1750 1770 1790  
GTGCTCTACCAGTGAAGCTAAATCTCCAACCCCTGAAGGCCTCTTTCTTTCTGCCTCTGAT  
1810 1830 1850  
AGTCTATGACATTCTTTTTTCTACAATTCGTATCAGGTGCACGAGCCTTATCCCATTGT  
1870 1890 1910  
AGGTTTCTAGGCAAGTTGACCGTTAGCTATTTTCCCTCTGAAGATTTGATTGAGTTGC  
1930 1950 1970  
AGACTTGGCTAGACAAGCAGGGGTAGGTTATGGTAGTTTATTTAACAGACTGCCACCAGG  
1990 2010 2030  
AGTCCAGTGTCTTCTGTTCTCTGTAGTTGTACCTAAGCTGACTCCAAGTACATTTAGTA  
2050 2070 2090  
TGAAAATAATCAACAAATTTTATTCTCTATCAACATTGGCTAGCTTTGTTTCAGGGC  
2110 2130 2150  
ACTAAAAGAACTACTATATGGAGAAAGAAATTGATATTGCCCCAACGTTCAACAACCCA  
2170 2190 2210  
ATAGTTTATCCAGCTGTCATGCCTGGTTCAGTGTCTACTGACTATGCGCCCTCTTATTAC  
2230 2250 2270  
TGCATGCAGTAATTCAACTGGAAATAGTAATAATAATAATAGAAATAAAATCTAGACTCC  
2290 2310 2330  
ATTGGATCTCTCTGAATATGGGAATATCTAACTTAAGAAGCTTTGAGATTTCAAGTTGTGT  
2350 2370 2390  
TAAAGGCTTTTATTAAAAAGCTGATGCTCTTCTGTAAAAGTTACTAATATATCTGTAAGA  
2410 2430

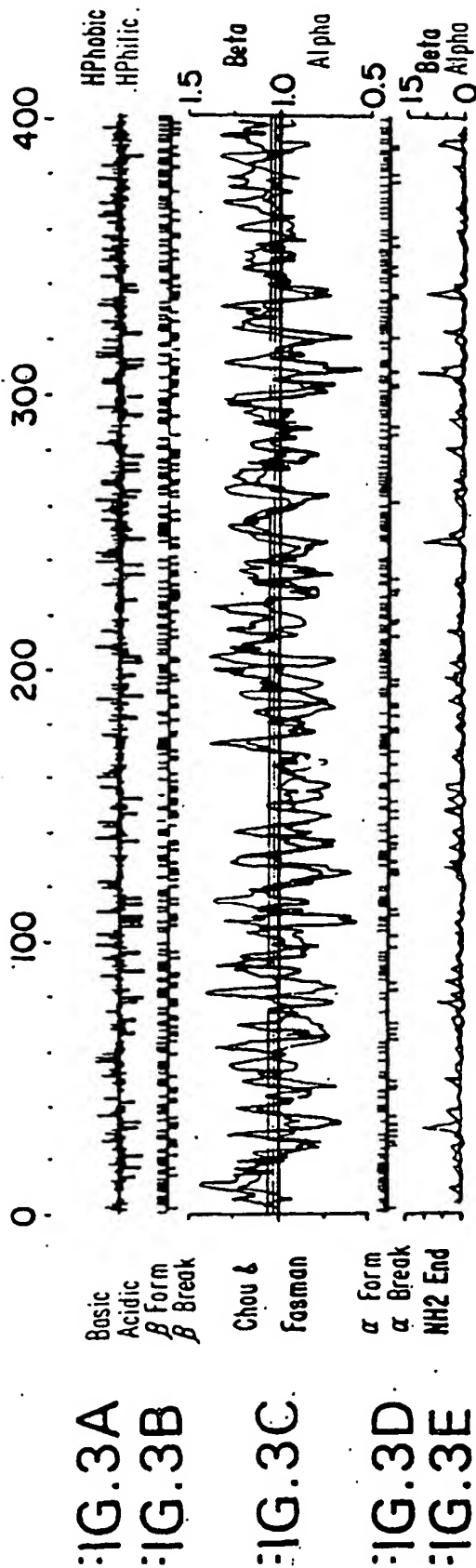














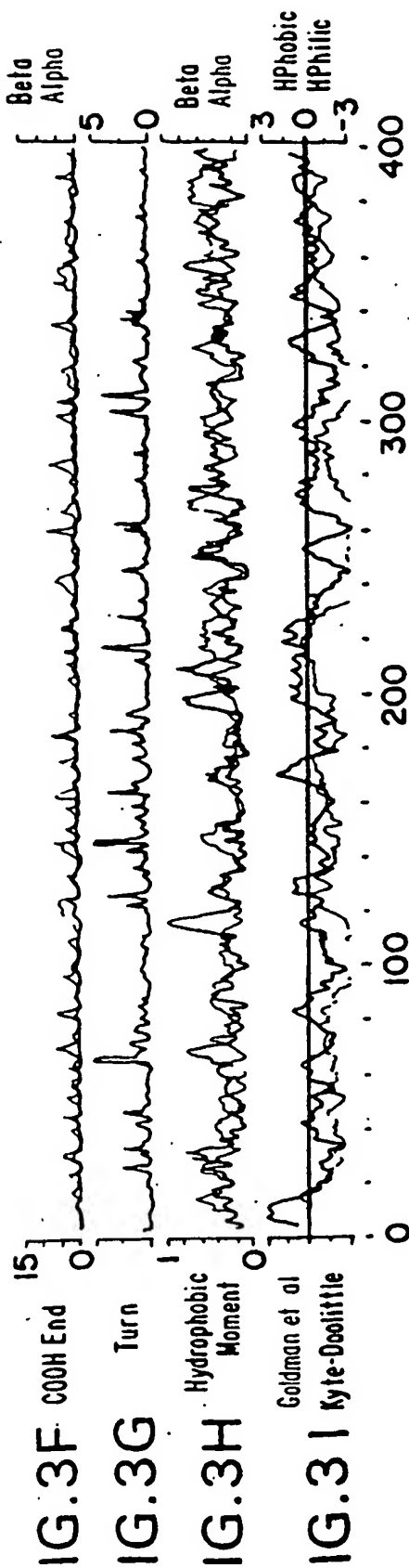




FIG. 4A

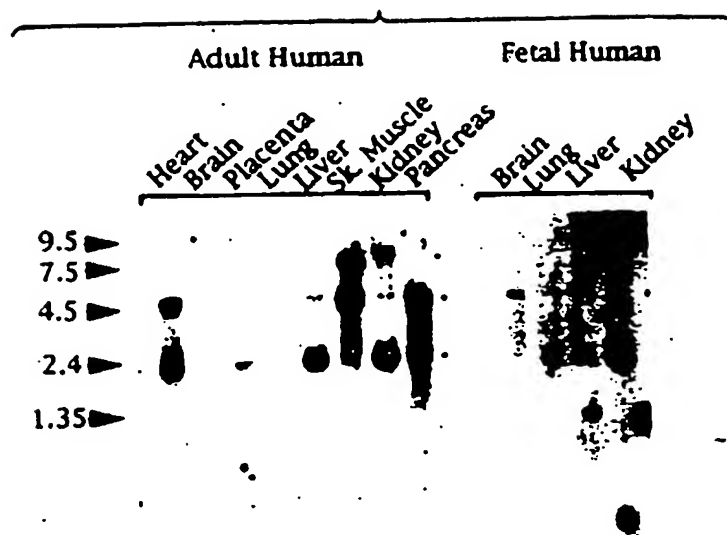


FIG. 4B

Human Immune System

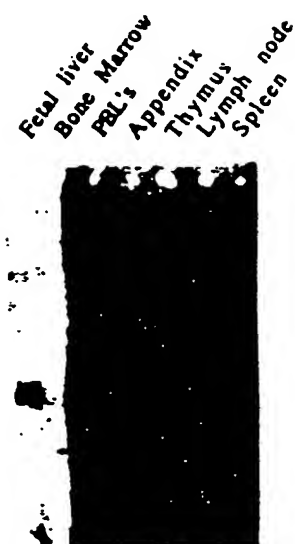




FIG.5

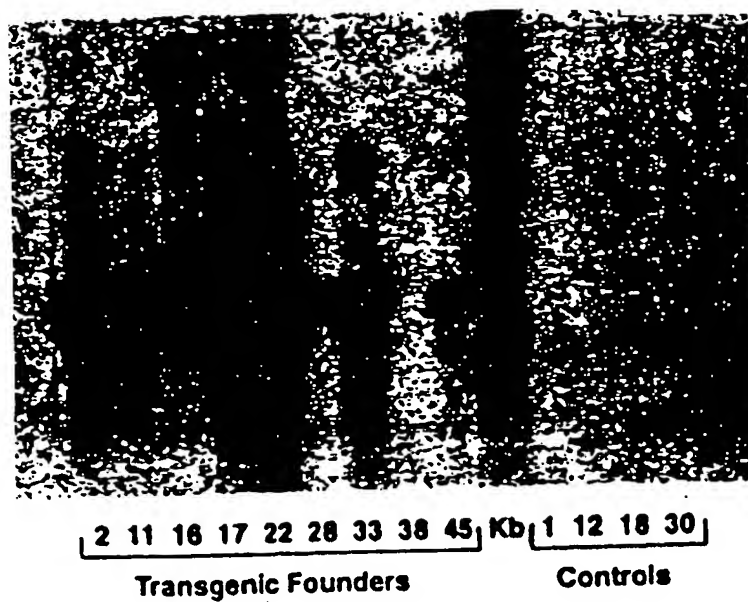




FIG.6A



FIG.6B

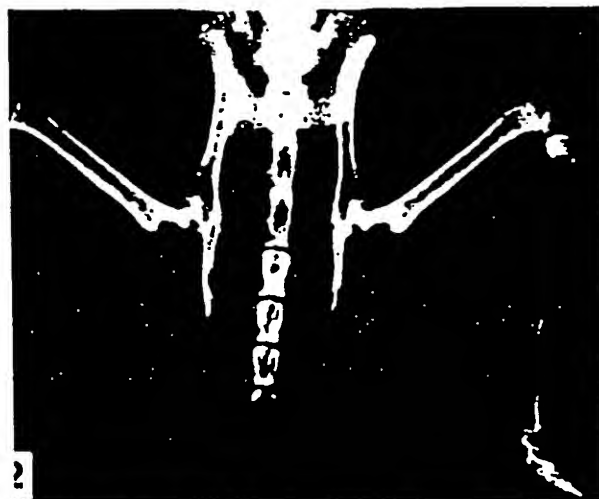


FIG.6C

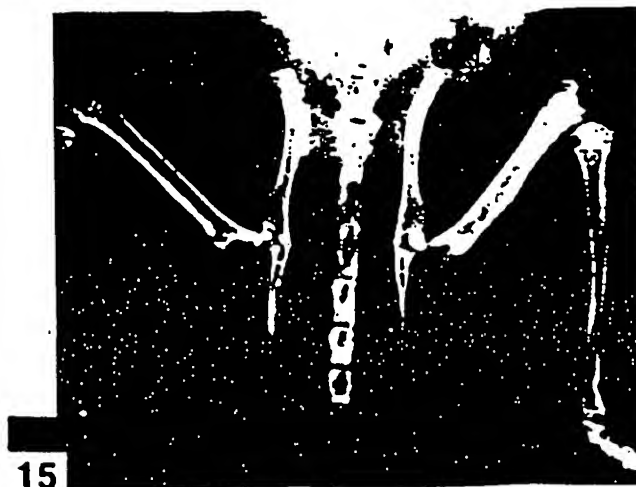




FIG. 6D

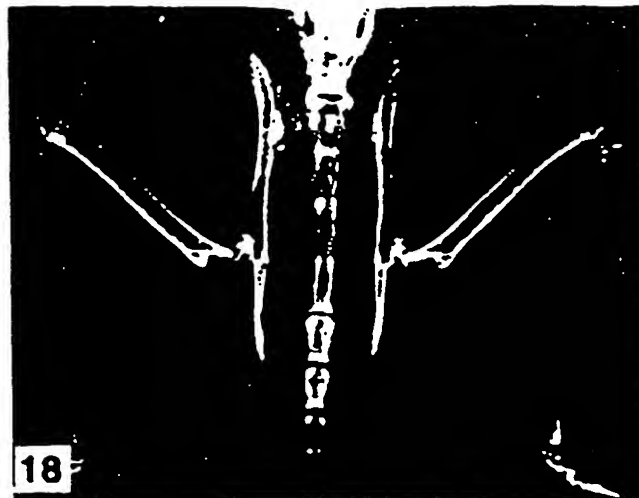


FIG. 6E



FIG. 6F

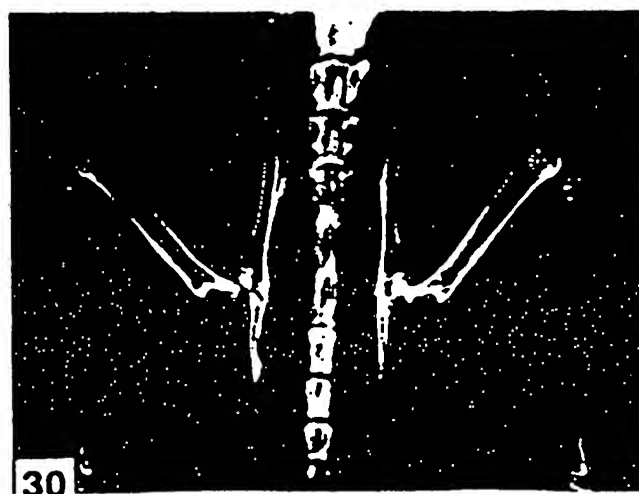




FIG.6G



FIG.6H

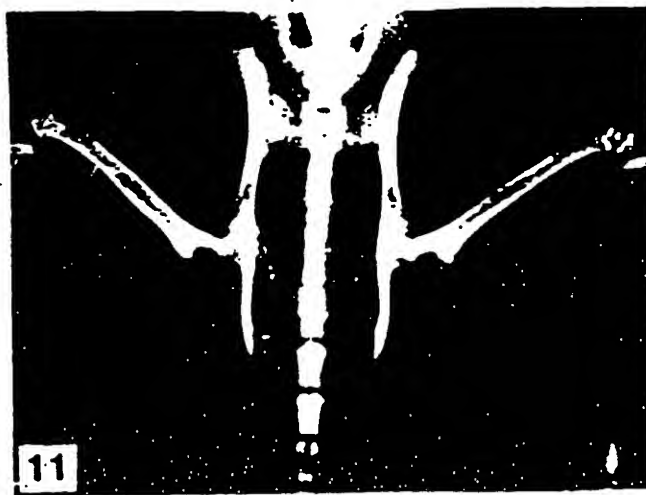




FIG.6I



FIG.6J





FIG.7A



FIG.7B



FIG.7C

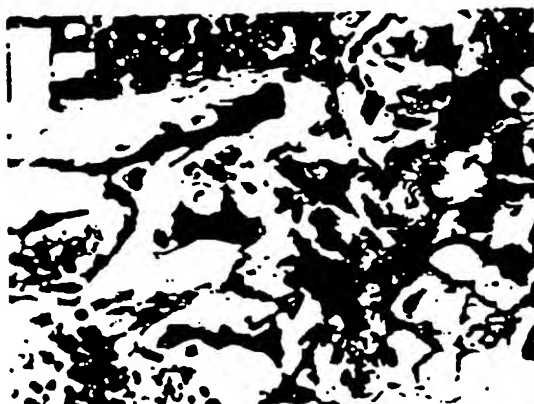


FIG.7D





FIG.7E

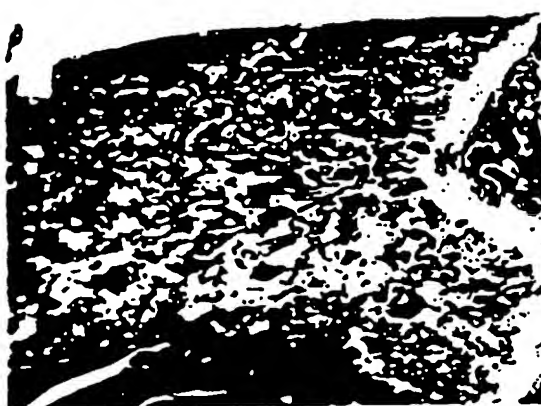


FIG.7F

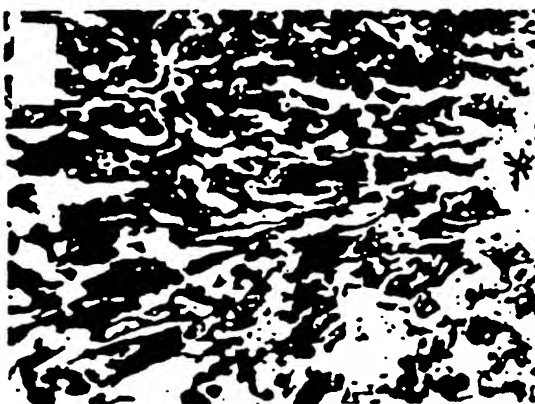


FIG.7G

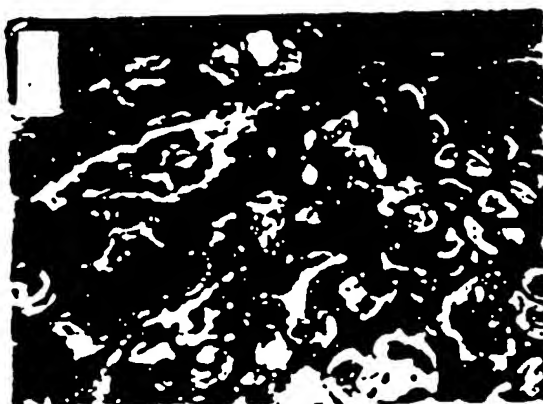


FIG.7H





FIG.8A



FIG.8B

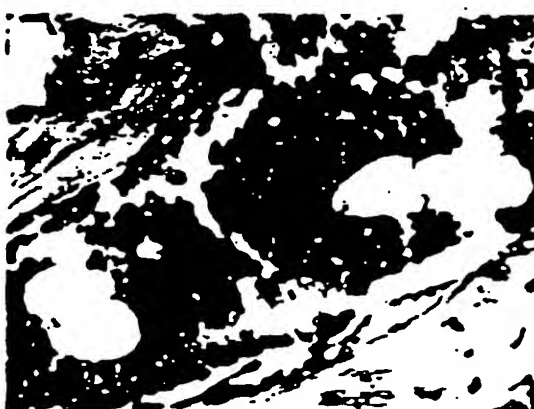
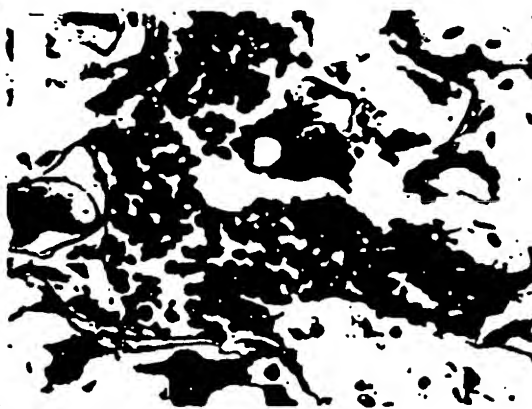


FIG.8C



FIG.8D





## FIG.9A

10 30 50  
CCTTATATAARACGTCATGATTGCCTGGGCTGCAGAGACGCACCTAGCACTGACCCAGCG  
70 90 110  
GCTGCCTCCTGAGGTTTCCCGAGGACCACAATGAACAAGTGGCTGTGCTGCGCACTCCTG  
M N K W L C C A L L  
130 150 170  
GTGCTCCTGGACATCATTGAATGGACAACCCAGGAAACCCTTCCTCCAAAGTACTTG CAT  
V L L D I L E W T T O E T L P P K Y L H  
190 210 230  
TATGACCCAGAACTGGTCATCAGCTCC'GTGTGACAAATGTGCTCCTGGCACCTACCTA  
Y D P E T G H Q L L C D K C A P G T Y L  
250 270 290  
AAACAGCACTGCACAGTGAGGAGGAAGACATTGTGTGTCCCTTGCCCTGACCACTCTTAT  
K Q H C T V R R K T L C V P C P D H S Y  
310 330 350  
ACGGACAGCTGGCACACCAGTGATGAGTGTGTGTATTGCAGCCCAGTGTGCAAGGAACTG  
T D S W H T S D E C V Y C S P V C K E L  
370 390 410  
CAGTCCGTGAAGCAGGAGTGCAACCGCACCCACAACCGAGTGTGTGAGTGTGAGGAAGGG  
Q S V K Q E C N R T H N R V C E C E E G  
430 450 470  
CGTTACCTGGAGATCGAATTCTGCTTGAAGCACCGGAGCTGTCCCCCGGGCTCCGGCGTG  
R Y L E I E F C L K H R S C P P G S G V  
490 510 530  
GTGCAAGCTGGAACCCCAGAGCGAAACACAGTTTGCAAAAAATGTCCAGATGGGTTCTTC  
V Q A G T P E R N T V C K K C P D G F F  
550 570 590  
TCAGGTGAGACTTCATCGAAAGCACCCCTGTATAAAACACACGAACTGCAGCACATTGCGC  
S G E T S S K A P C I K H T N C S T F G  
610 630 650  
CTCCTGCTAATTCAGAAAGGAAATGCAACACATGACAACGTGTGTTCGGAAACAGAGAA  
L L L I Q K G N A T H D N V C S G N R E  
670 690 710  
GCCACGCAAAAGTGTGGAATAGATGTCACCCTGTGTGAAGAGGCCTTCTTCAGGTTTGCT  
A T Q K C G I D V T L C E E A F F R F A  
730 750 770  
GTTCTACCAAGATTATACCAAATGGCTGAGTGT'TTGGTGGACAGTTTGCCTGGGACC  
V P T K I I P N W L S V L V D S L P G T



## FIG.9B

790 810 830  
AAAGTGAATGCCGAGAGTGTAGAGAGGATAAAACGGAGACACAGCTCACAAGAGCAAACC  
K V N A E S V E R I K R R H S S Q E Q T  
850 870 890  
TTCCAGCTGCTGAAGCTGTGGAACATCAAAACAGAGACCAGGAAATGGTGAAGAAGATC  
F Q L L K L W K H Q N R D Q E M V K K I  
910 930 950  
ATCCAAGACATTGACCTCTGTGAAAGCAGCGTGCAGCGGCATCTCGGCCACTCGAACCTC  
I Q D I D L C E S S V Q R H L G H S N L  
970 990 1010  
ACCACAGAGCAGCTTCTTGCCTTGATGGAGAGCCTGCCTGGGAAGAAGATCAGCCCAGAA  
T T E Q L L A L M E S L P G K K I S P E  
1030 1050 1070  
GAGATTGAGAGAACGAGAAAGACCTGCAAATCGAGCGAGCAGCTCCTGAAGCTACTCAGT  
E I E R T R K T C K S S E Q L L K L L S  
1090 1110 1130  
TTATGGAGGATCAAAAATGGTGACCAAGACACCTTGAAGGGCCTGATGTATGCCCTCAAG  
L W R I K N G D Q D T L K G L M Y A L K  
1150 1170 1190  
CACTTGAAAACATCCCACCTTCCCAAACTGTCACCCACAGTCTGAGGAAGACCATGAGG  
H L K T S H F P K T V T H S L R K T M R  
1210 1230 1250  
TTCTGCACAGCTTCACAATGTACAGACTGTATCAGAAGCTCTTTTTAGAAATGATAGGG  
F L H S P T M Y R L Y Q K L F L E M I G  
1270 1290 1310  
AATCAGGTTCAATCCGTGAAAATAAGCTGCTTATAACTAGGAATGGTCACTGGGCTGTTT  
N Q V Q S V K I S C L

CTTCA



## FIG. 9C

10 30 50  
GTATATATAACGTGATGAGCGTACGGGTGCGGAGACGCACCGGAGCGCTCGCCCAGCCGC  
70 90 110  
CGYCTCCAAGCCCCCTGAGGTTTCCGGGGACCACAATGAACAAGTTGCTGTGCTGCGCGCT  
130 150 170  
CGTGTCTTCTGGACATCTCCATTAAGTGGACCAACCAGGAAACGTTTCCTCCAAAGTACCT  
V F L D I S I K W T T O E T P P P K Y L  
190 210 230  
TCATTATGACGAAGAAACCTCTCATCAGCTGTTGTGTGACAAATGTCCTCCTGGTACCTA  
H Y D E E T S H Q L L C D K C P P G T Y  
250 270 290  
CCTAAACAACACTGTACAGCAAAGTGAAGACCGTGTGCGCCCCTTGCCCTGACCACTA  
L K Q H C T A K W K T V C A P C P D H Y  
310 330 350  
CTACACAGACAGCTGGCACACCCAGTGACGAGTGTCTATACTGCAGCCCCGTGTGCAAGGA  
Y T D S W H T S D E C L Y C S P V C K E  
370 390 410  
GCTGCAGTACGTCAAGCAGGAGTGCAATCGCACCCACAACCGCGTGTGCAATGCAAGGA  
L Q Y V K Q E C N R T H N R V C E C K E  
430 450 470  
AGGGCGCTACCTTGAGATAGAGTTCTGCTTGAAACATAGGAGCTGCCCTCCTGGATTG  
G R Y L E I E F C L K H R S C P P G F G  
490 510 530  
AGTGGTGCAAGCTGGAACCCAGAGCGAAATACAGTTTGCAAAAGATGTCCAGATGGGTT  
V V Q A G T P E R N T V C K R C P D G F  
550 570 590  
CTTCTCAAATGAGACGTCATCTAAAGCACCTGTAGAAAACACACAAATTGCAGTGTCTT  
F S N E T S S K A P C R K H T N C S V F  
610 630 650  
TGGTCTCCTGCTAACTCAGAAAGGAAATGCAACACACGACAACATATGTTCCGGAAACAG  
G L L L T Q K G N A T H D N I C S G N S  
670 690 710  
TGAATCAACTCAAAAATGTGGAATAGATGTTACCCTGTGTGAGGAGGCATTCTTCAGGTT  
E S T Q K C G I D V T L C E E A F F R F  
730 750 770  
TGCTGTTCTTACAAAGTTTACGCCTAACTGGCTTAGTGTCTTGCTAGACAATTTGCCTGG  
A V P T K F T P N W L S V L V D N L P G



## FIG.9D

790 810 830  
CACCAAAGTAAACGCAGAGAGTGTAGAGAGGATAAAACGGCAACACAGCTCACAAGAACA  
T K V N A E S V E R I K R Q H S S Q E Q  
850 870 890  
GACTTTCAGCTGCTGAAGTTATGGAAACATCAAAACAAAGACCAAGATATAGTCAAGAA  
T F Q L L K L W K H Q N K D Q D I V K K  
910 930 950  
GATCATCCAAGATATTGACCTCTGTGAAAACAGCGTGCAGCGGCACATTGGACATGCTAA  
I I Q D I D L C E N S V Q R H I G H A N  
970 990 1010  
CCTCACCTTCGAGCAGCTTCGTAGCTTGATGGAAAGCTTACCGGGAAAGAAAGTGGGAGC  
L T F E Q L R S L M E S L P G K K V G A  
1030 1050 1070  
AGAAGACATTGAAAAACAATAAAGGCATGCAAACCCAGTGACCAGATCCTGAAGCTGCT  
E D I E K T I K A C K P S D Q I L K L L  
1090 1110 1130  
CAGTTTGTGGCGAATAAAAAATGGCGACCAAGACACCTTGAAGGGCCTAATGCACGCACT  
S L W R I K N G D Q D T L K G L M H A L  
1150 1170 1190  
AAAGCACTCAAAGACGTACCACTTTCCCAAAACTGTCACTCAGAGTCTAAAGAAGACCAT  
K H S K T Y H P P K T V T Q S L K K T I  
1210 1230 1250  
CAGGTTCCTTCACAGCTTCACAATGTACAAATTGTATCAGAAGTTATTTTATAGAAATGAT  
R F L H S F T M Y K L Y Q K L F L E M I  
1270 1290 1310  
AGGTAACCAGGTCCAATCAGTAAAAATAAGCTGCTTATAACTGGAAATGGCCATTGAGCT  
G N Q V Q S V K I S C L  
1330 1350  
GTTTCCTCACAATTGGCGAGATCCCATGGATGATAA



FIG. 9E

muosteo.frg	MNKNLCCALLVLLDIIIEWTTQETLPPKYYLHYDPEETGHQLLCLCDKCAPGGTYL	50
ratosteo.frg	MNKNLCCALLVLLDIIIEWTTQETLPPKYYLHYDPEETGRQLLCLCDKCAPGGTYL	50
huosteo.frg	MNKNLCCALLVFLDISIRWTTQETLPPKYYLHYDEETSHQLLCLCDKCAPGGTYL	50
muosteo.frg	KQHCTVRRKTL CVPCPDH SYTDSWHTSDECVYCS PVCKELQSVKQECNRT	100
ratosteo.frg	KQHCTVRRKTL CVPCPDY SYTDSWHTSDECVYCS PVCKELQSVKQECNRT	100
huosteo.frg	KQHCTAKWKTVCAPCPDH Y Y TDSWHTSDECLYCS PVCKELQSVKQECNRT	100
muosteo.frg	HN RVCECEEGRYLEIEFCCLKHRS CPPGSGV VQA GTPEERN TVCKKCPDGGFF	150
ratosteo.frg	HN RVCECEEGRYLEIEFCCLKHRS CPPGSLGV LQA GTPEERN TVCKRCPDGGFF	150
huosteo.frg	HN RVCECKEGRYLEIEFCCLKHRS CPPPGFVQA GTPEERN TVCKRCPDGGFF	150
muosteo.frg	SGETSSSKAPCIKHHTNCS TFGLLLLIQKGNATHBDNVCSGNGREATAQKCGIDVT	200
ratosteo.frg	SGETSSSKAPCRKHHTNCS S LGLLLLIQKGNATHBDNVCSGNGREATAQNCGIDVT	200
huosteo.frg	SHETSSSKAPCRKHHTNCS V FGLLLLTQKGNATHBDNICSNGNSESTQKCGIDVT	200



**FIG. 9F**

muosteo.frg	L	C	E	E	A	F	F	R	F	A	V	P	T	K	I	I	P	N	W	L	S	V	L	V	D	S	L	P	G	T	K	V	N	A	E	S	V	E	R	I	K	R	R	H	S	S	S	Q	E	Q	T	250	
ratosteo.frg	L	C	E	E	A	F	F	R	F	A	V	P	T	K	I	I	P	N	W	L	S	V	L	V	D	S	L	P	G	T	K	V	N	A	E	S	V	E	R	I	K	R	R	H	S	S	S	Q	E	Q	T	250	
huosteo.frg	L	C	E	E	A	F	F	R	F	A	V	P	T	K	I	F	T	P	N	W	L	S	V	L	V	D	N	L	P	G	T	K	V	N	A	E	S	V	E	R	I	K	R	Q	H	S	S	S	Q	E	Q	T	250

muosteo.frg	F	Q	L	L	K	K	Q	N	R	D	Q	E	M	V	K	K	I	I	Q	D	I	D	L	C	E	S	S	V	Q	R	H	L	G	H	S	N	L	T	T	E	Q	L	L	A	L	M	E
ratosteo.frg	F	Q	L	L	K	K	Q	N	R	D	Q	E	M	V	K	K	I	I	Q	D	I	D	L	C	E	S	S	V	Q	R	H	I	G	H	A	N	L	T	T	E	Q	L	R	I	L	M	E
huosteo.frg	F	Q	L	L	K	K	Q	N	R	D	Q	D	I	V	K	K	I	I	Q	D	I	D	L	C	E	N	S	V	Q	R	H	I	G	H	A	N	L	T	F	E	Q	L	R	S	L	M	E

muesteo.frg	S L P G K K I S P E E I E R T R K T C K S	S E Q L L K L L S L W R I K N G D Q D T L K G L M Y A L K	350
ratosteo.frg	S L P G K K I S P D E I E R T R K T C K P	S E Q L L K L L S L W R I K N G D Q D T L K G L M Y A L K	350
huosteo.frg	S L P G K K V G A E D I E R T I K A C K P S D Q	T L K L L S L W R I K N G D Q D T L K G L M H A L K	350

·muosteo. f.ig	H L K T S H F P K T V T H S L R K K T M	R F L B S F T M Y R L Y Q K L F L E M I G N Q V Q S V K I S C	400
ratosteo. f.ig	H L K A Y H F P K T V T H S L R K K T I R F L B S F T M Y R L Y Q K L F L E M I G N Q V Q S V K I S C	400	
·huosteo. f.ig	H S K T Y H F P K T V T Q S L K R K K T I R F L B S F T M Y R L Y Q K L F L E M I G N Q V Q S V K I S C	400	

muosteo.frg	L	401
ratosteo.frg	L	401
huosteo.frg	L	401



FIG.10

ltnrr	C	P	Q	-	G	K	Y	I	H	P	Q	N	N	S	I	C	C	T	K	C	H	K	G	T	Y	L	Y	N	D	C	P	G	P	G	Q	D	T	D	C	R	E	C	E	S	G	S	F	T	A	S	49
humoste	P	P	K	Y	L	H	Y	D	E	E	T	S	H	Q	L	L	C	D	K	C	P	P	G	T	Y	L	K	Q	H	C	T	A	K	-	W	K	T	V	C	A	P	C	P	D	H	Y	Y	T	D	S	49
ltnrr	E	N	H	L	R	H	C	L	S	C	S	-	K	C	R	K	E	M	G	Q	V	E	I	S	S	C	T	V	D	R	D	T	V	C	G	C	R	K	N	Q	Y	R	H	Y	W	S	E	N	L	F	98
humoste	W	H	T	S	D	E	C	L	Y	C	S	P	V	C	-	K	E	L	Q	Y	V	K	-	Q	E	C	N	R	T	H	N	R	V	C	E	C	K	E	G	R	Y	L	E	I	-	-	E	-	F	93	
ltnrr	Q	C	F	N	C	S	L	C	L	N	G	-	T	V	H	L	S	C	Q	E	K	Q	N	T	V	C	T	-	C	H	A	G	F	F	L	R	E	-	-	-	N	E	C	V	S	C	139				
humoste	-	C	L	K	H	R	S	C	P	P	G	F	G	V	V	Q	A	G	T	P	E	R	N	T	V	C	K	R	C	P	D	G	F	F	S	N	E	T	S	S	K	A	P	C	R	K	H	139			



FIG. II

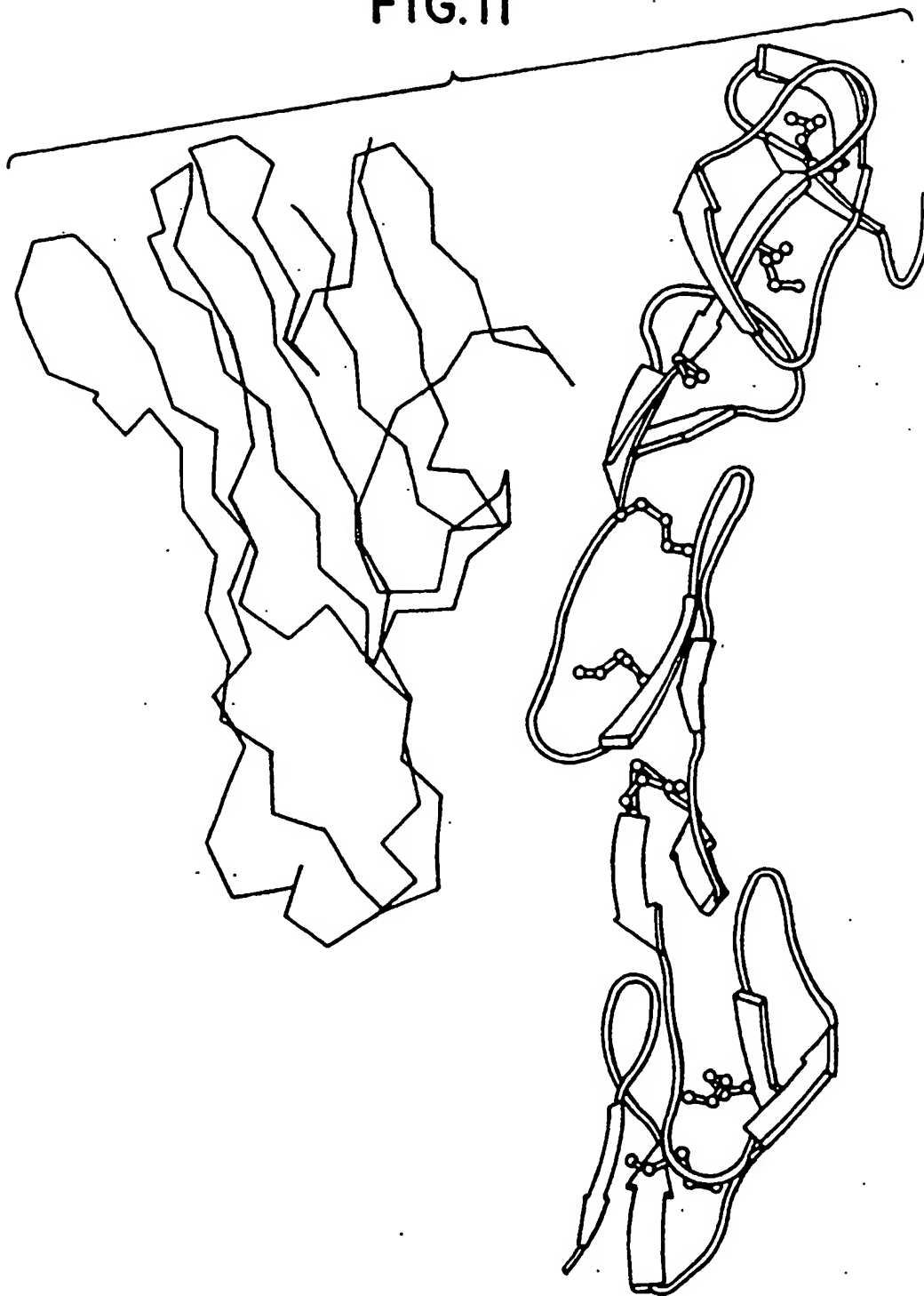




FIG. 12A

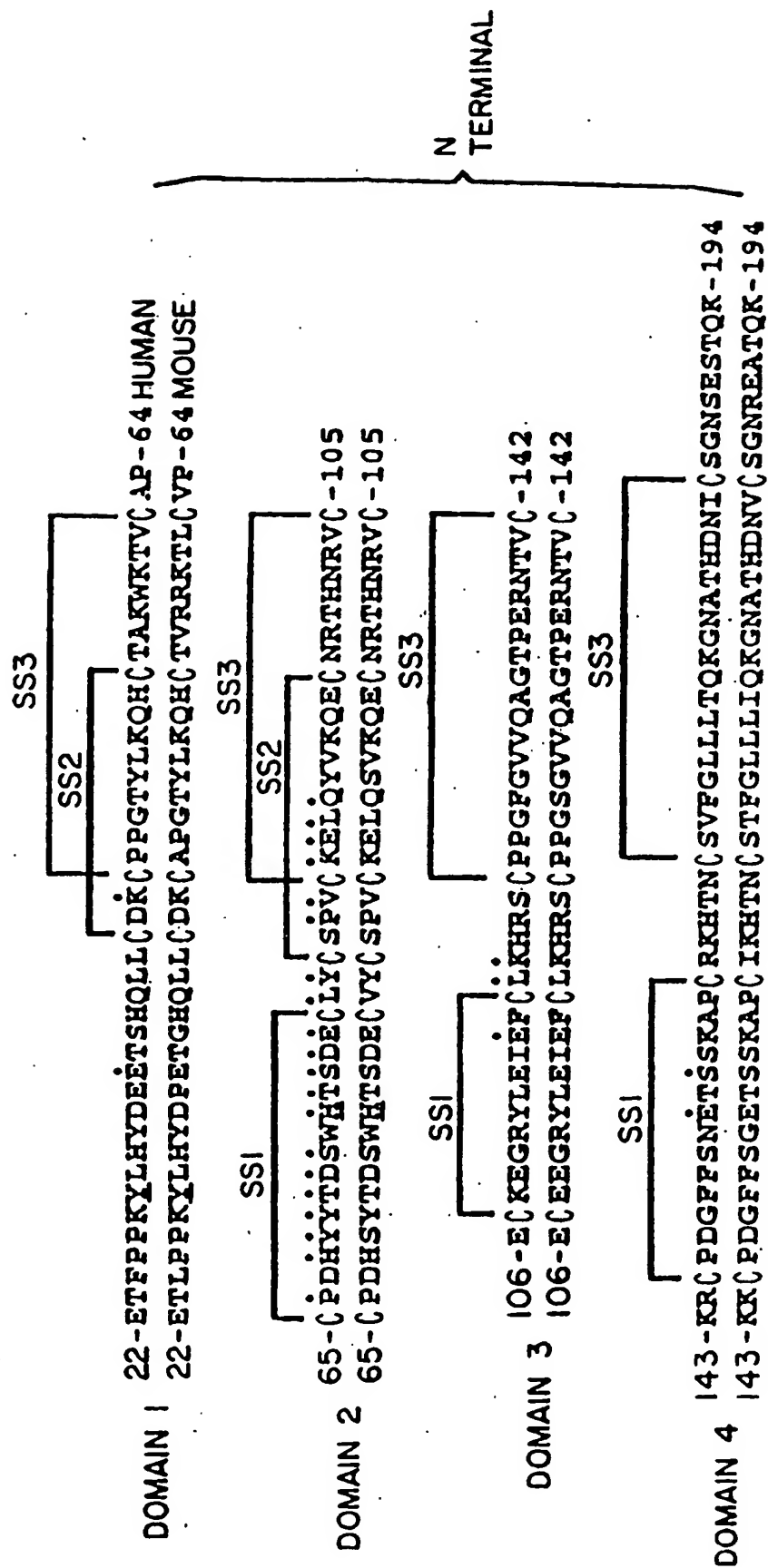




FIG. 12B

195-CGIDVTLC~~EE~~APFRPAVPTRKFTPNWLSVLVDNLPCTKVNAESVERIKRQHSS-246  
195-CGIDVTLC~~EE~~APFRPAVPTRKIIIPNWLSVLVDSLPGTKVNAESVERIKRRHSS-246  
247-QEOTFQLLLKWKHQNKDQDIVKKIIQDIDIL~~C~~ENSVQRHIGHANLTPEQLRSL-298  
247-QEOTFQLLLKWKHQNRDQEMVKKIIQDIDIL~~C~~ESSVQRHLGHSNLTTEQLLAL-298  
299-MESLPGKKVGAEDIEKTIKAC~~K~~PSDQILKLLSLWRIKNGDQDTLKGLMHALK-350  
299-MESLPGKKISP~~E~~IERTRKT~~C~~SS~~E~~QLLKLLSLWRIKNGDQDTLKGLMYALK-350  
351-HSKTYHPPKTVTQSLKKTIRFLHSFTMYKLYQKLPLEMIGNQVQSVKIS~~C~~L-401  
351-HLKTSHPPKTVTHSLRKTMRFLHSFTMYRLYQKLPLEMIGNQVQSVKIS~~C~~L-401

C  
TERMINAL



FIG.13A

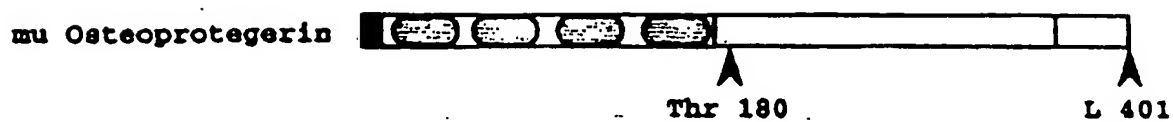


FIG.13B

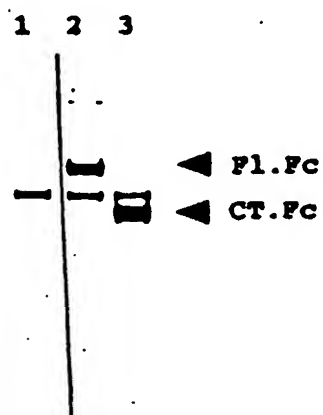


FIG.13C

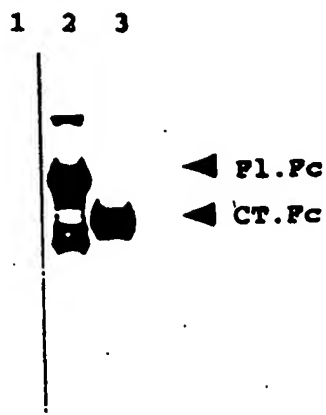




FIG.14A

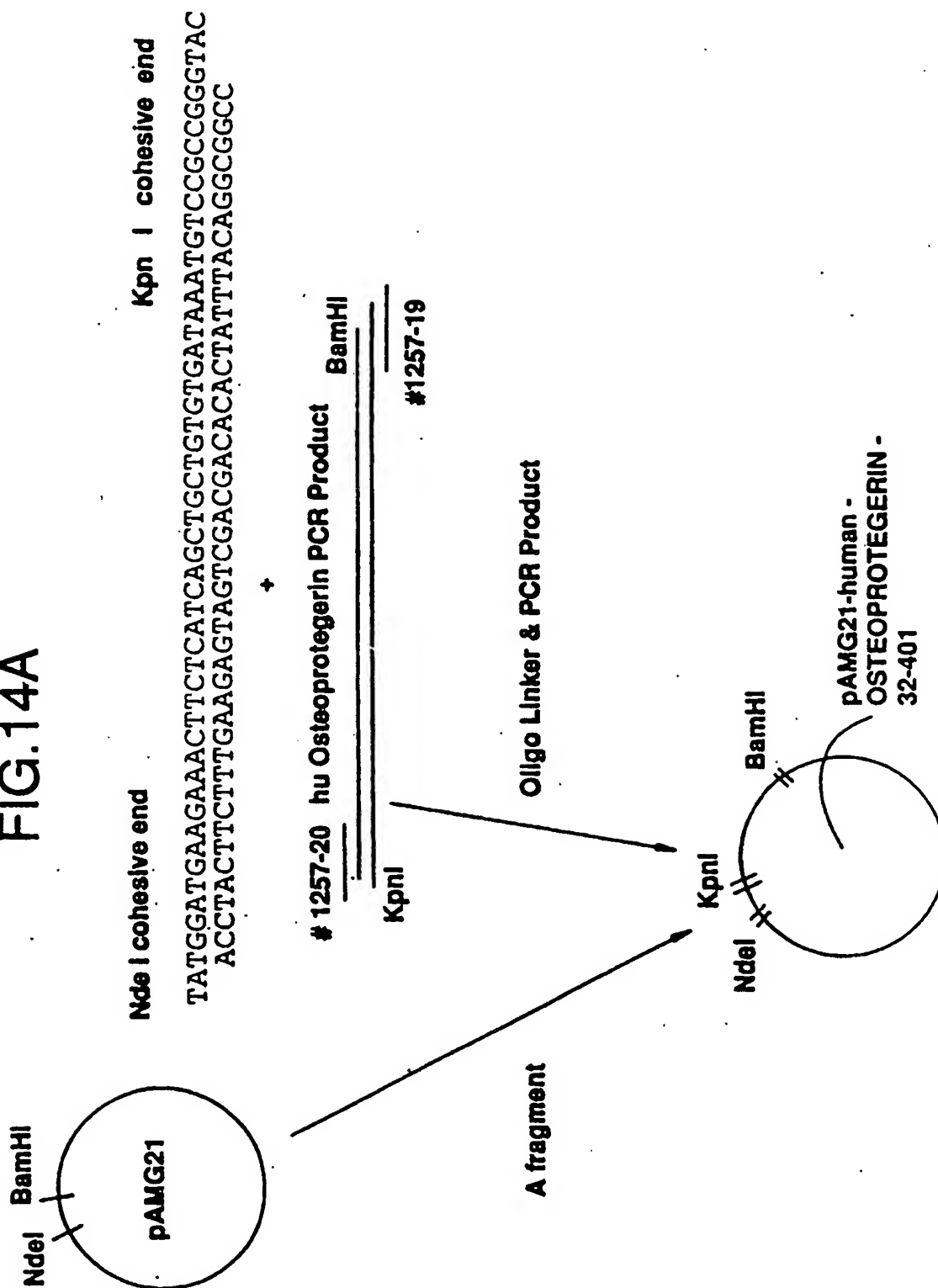




FIG. 14B

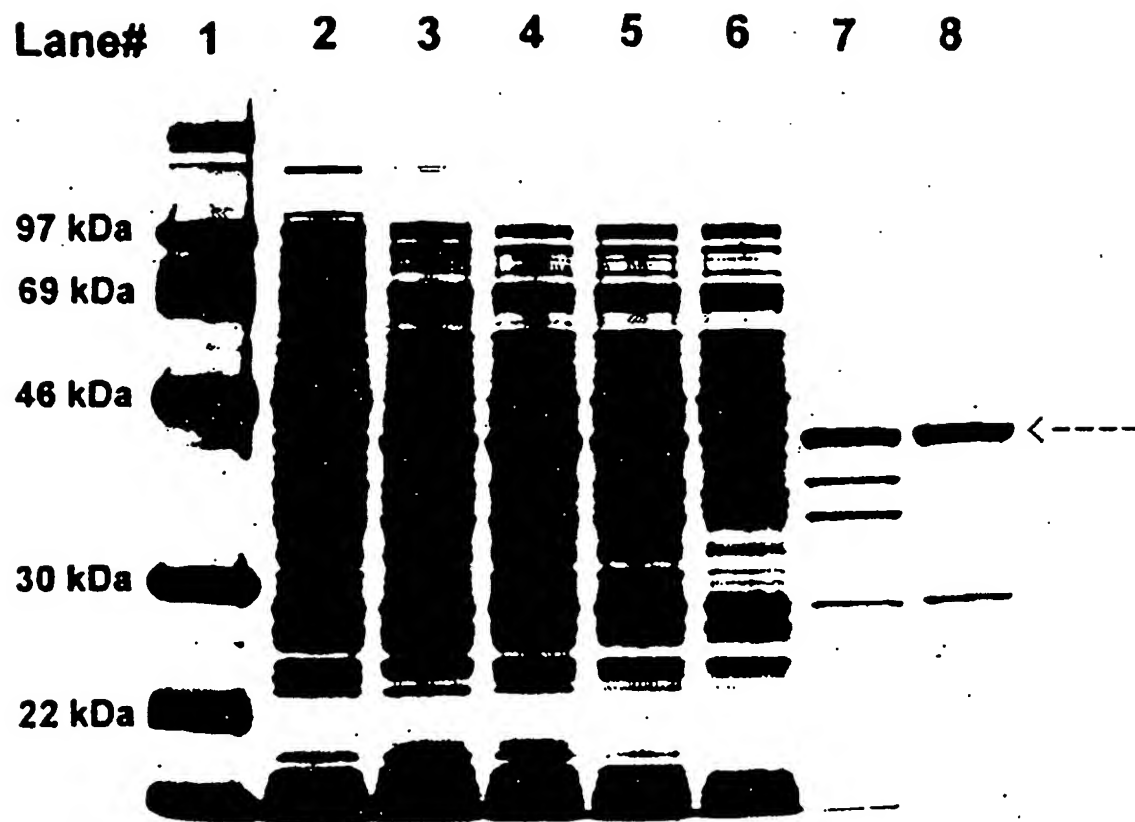




FIG. 15

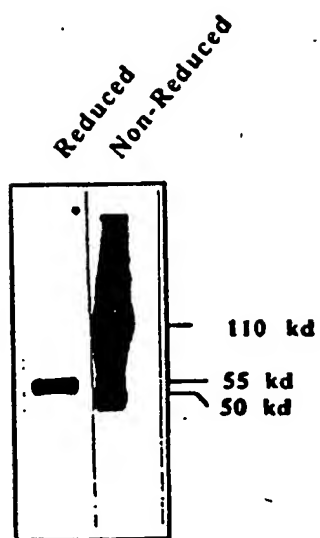




FIG.16A

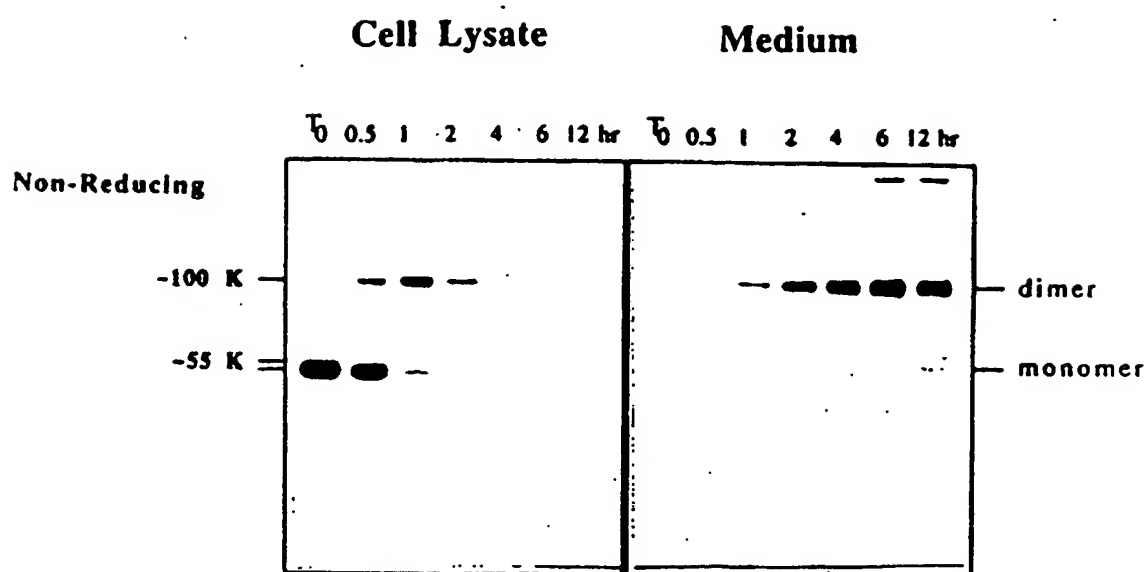


FIG.16B

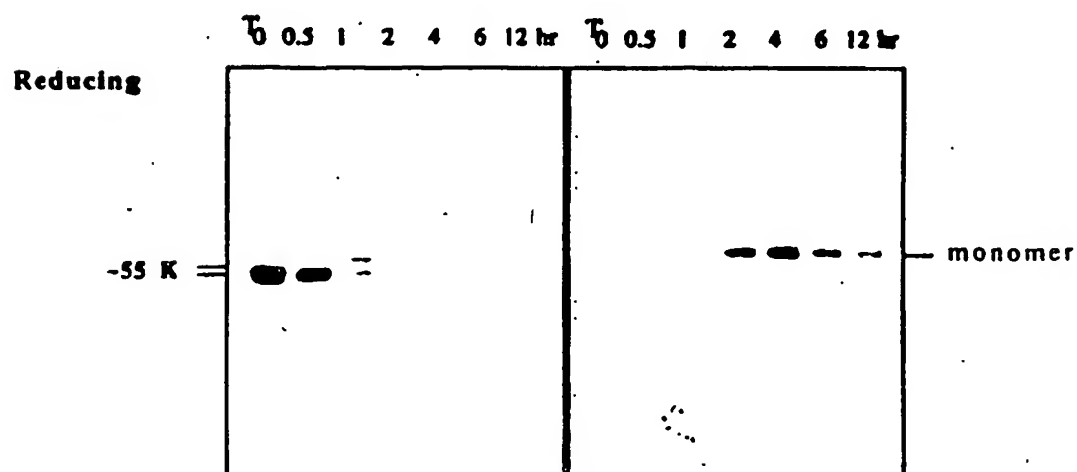




FIG. 17

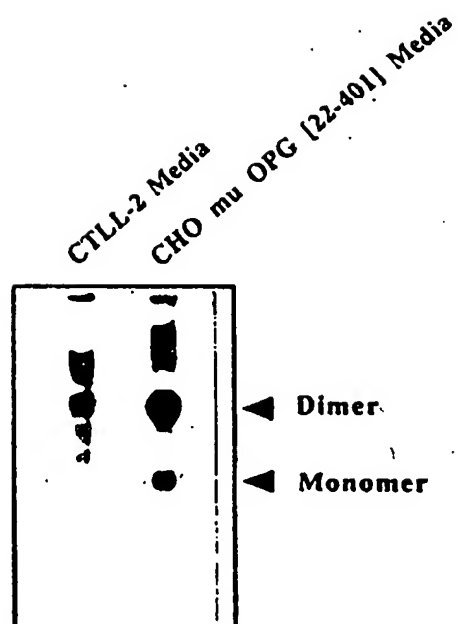








FIG.19A

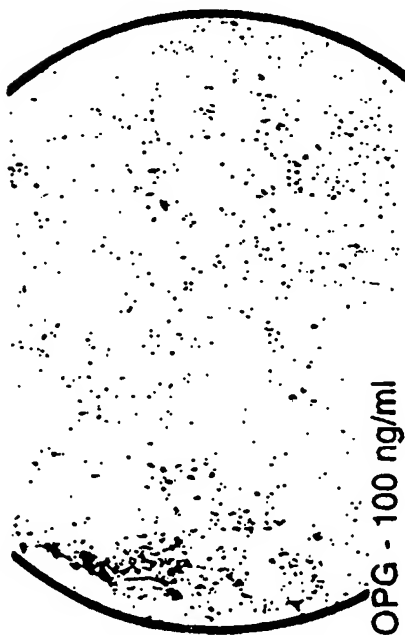


FIG.19B



FIG.19C

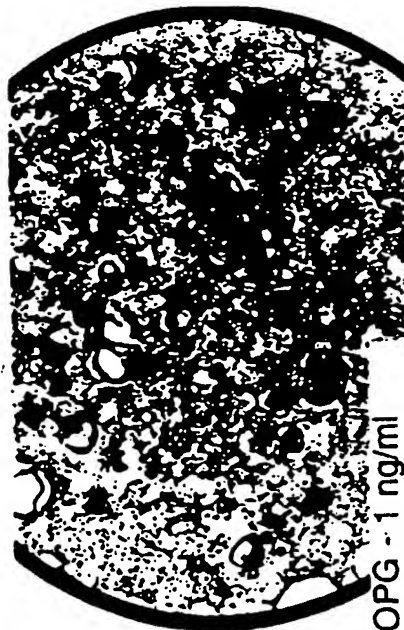


FIG.19D

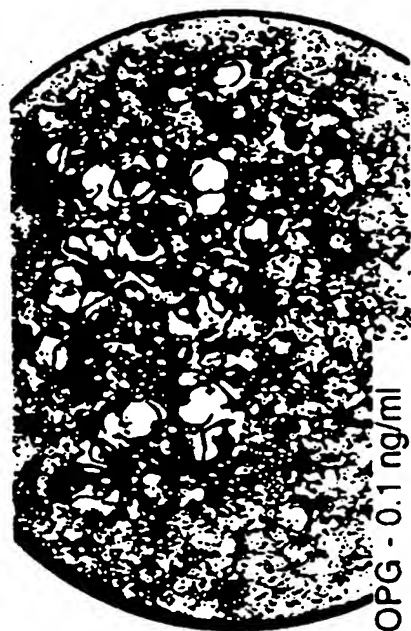




FIG.19E

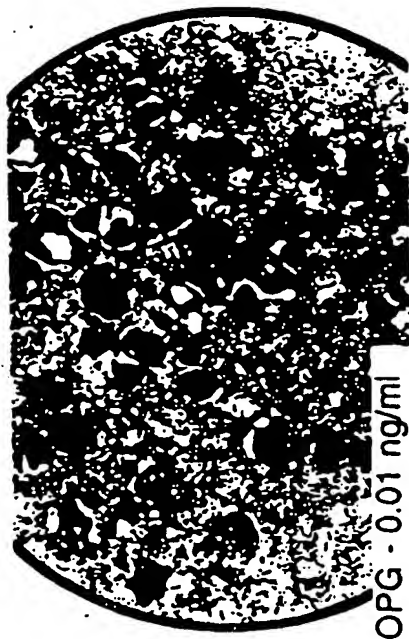


FIG.19F

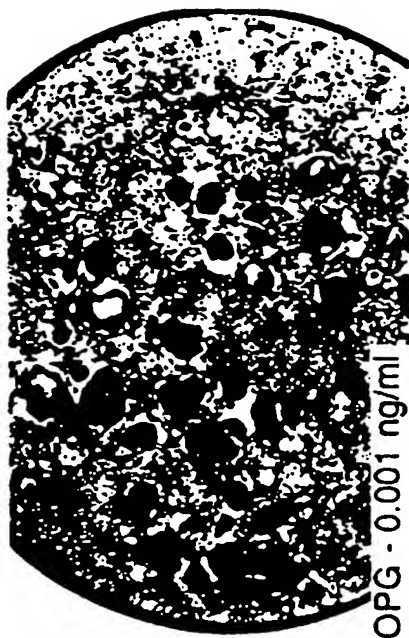


FIG.19G

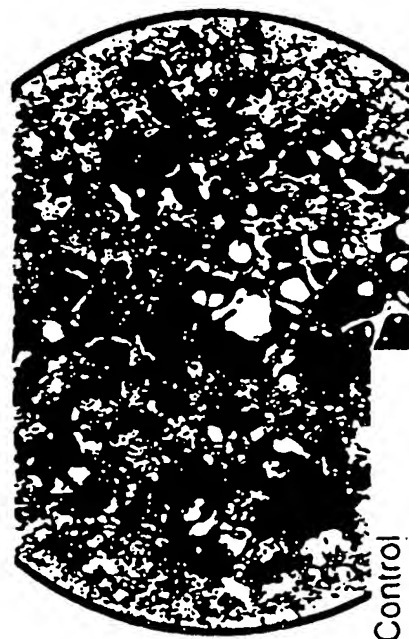




FIG.20

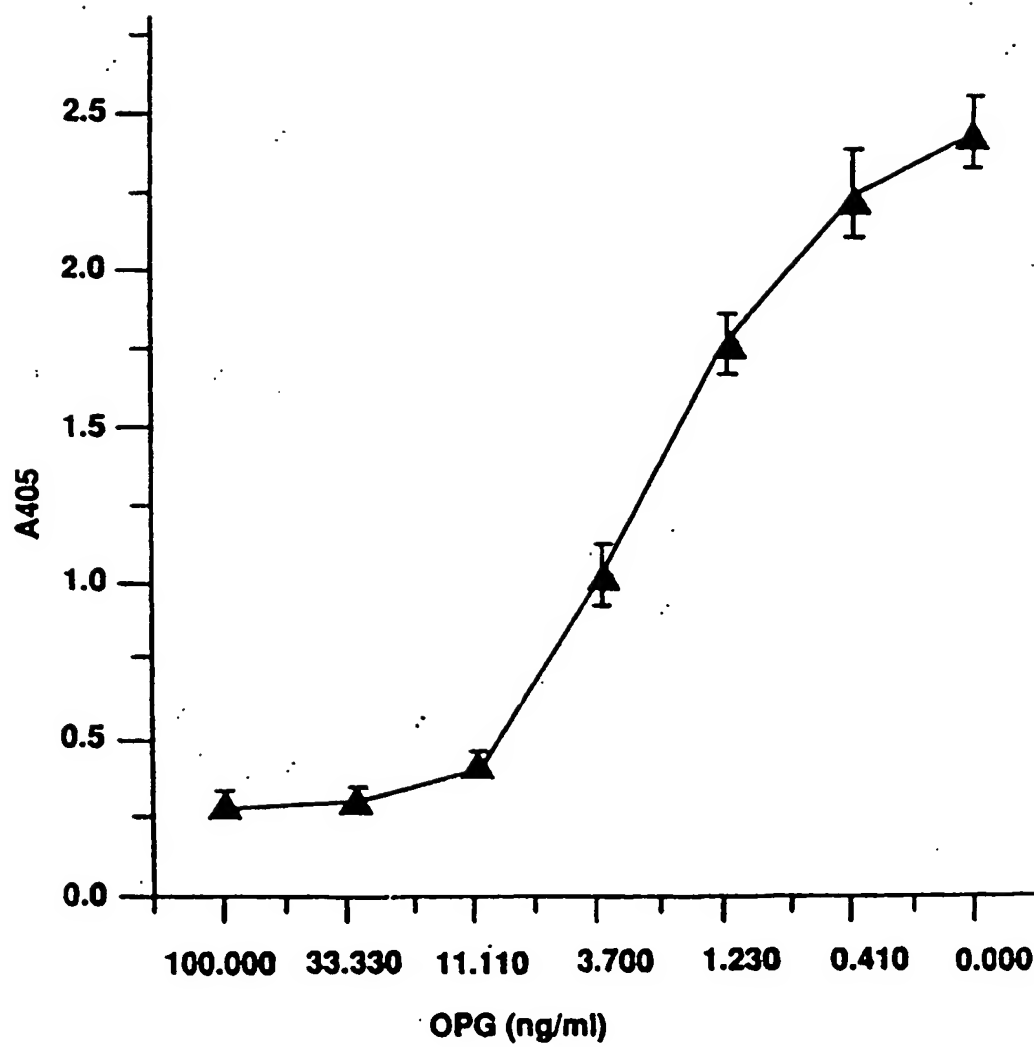
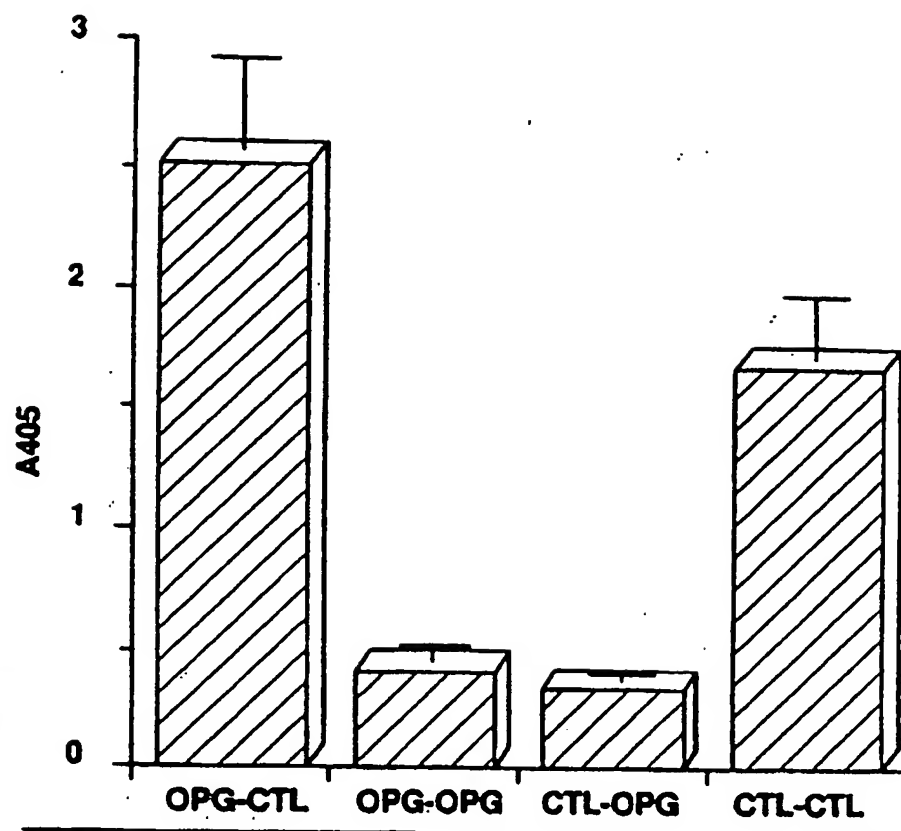




FIG.21



## Legend

**Growth**  
**Bone marrow**  
**cells**  
**CSF -1**

**Intermediate**  
**PGE2 + CSF-1**

**Terminal**  
**ST2 cells**  
**1,25 (OH)2 D3**  
**Dexamethasone**

4 days

2 days

8 - 10 days

## Groups

CTL - CTL

OPG - CTL

OPG - OPG

OPG - OPG

OPG

100 ng/ml

100 ng/ml

OPG

100 ng/ml

100 ng/ml



FIG.22A

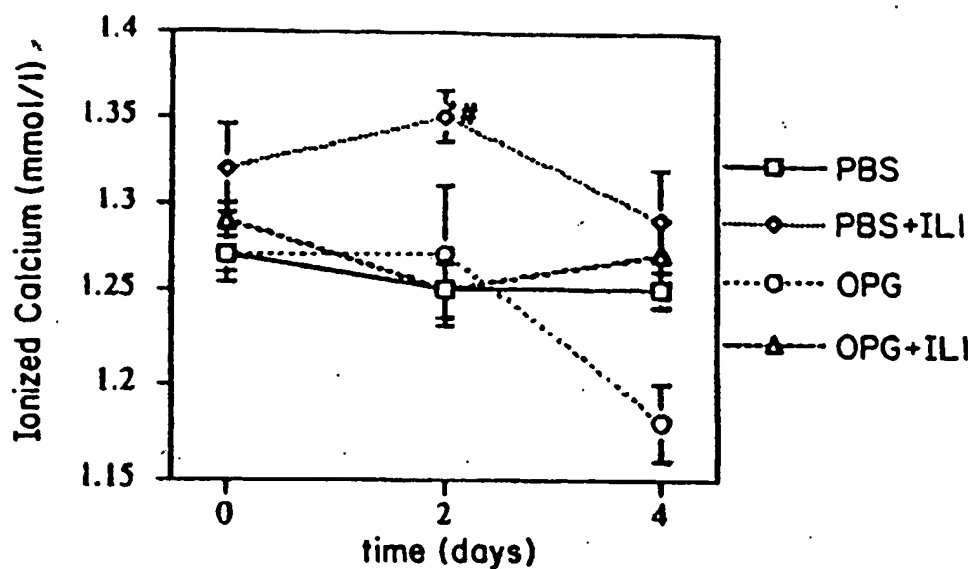
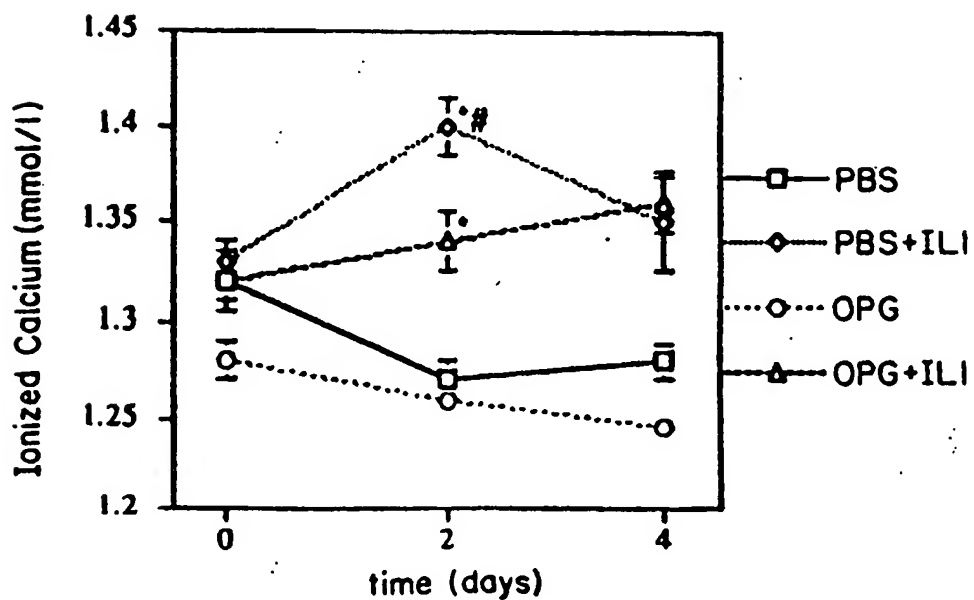


FIG.22B



\* Different to PBS,  $p < 0.05$

# Different to OPG + IL1,  $p < 0.05$



FIG.23A

PBS/PBS



FIG.23B





FIG.23C

PBS/OPG



FIG.23D

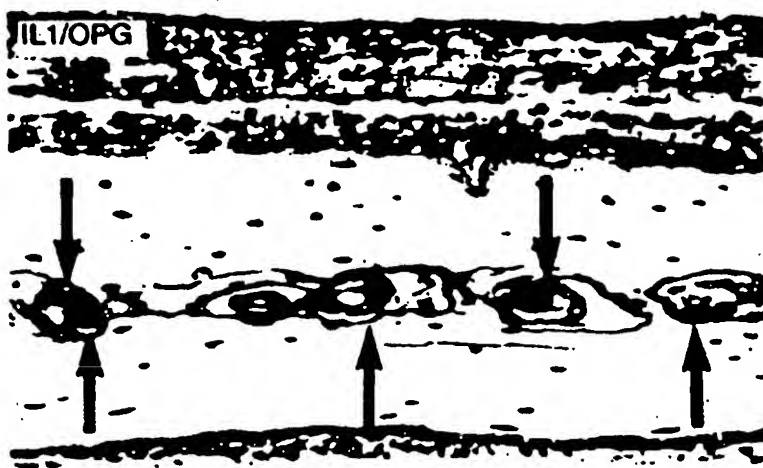




FIG. 24B



FIG. 24A

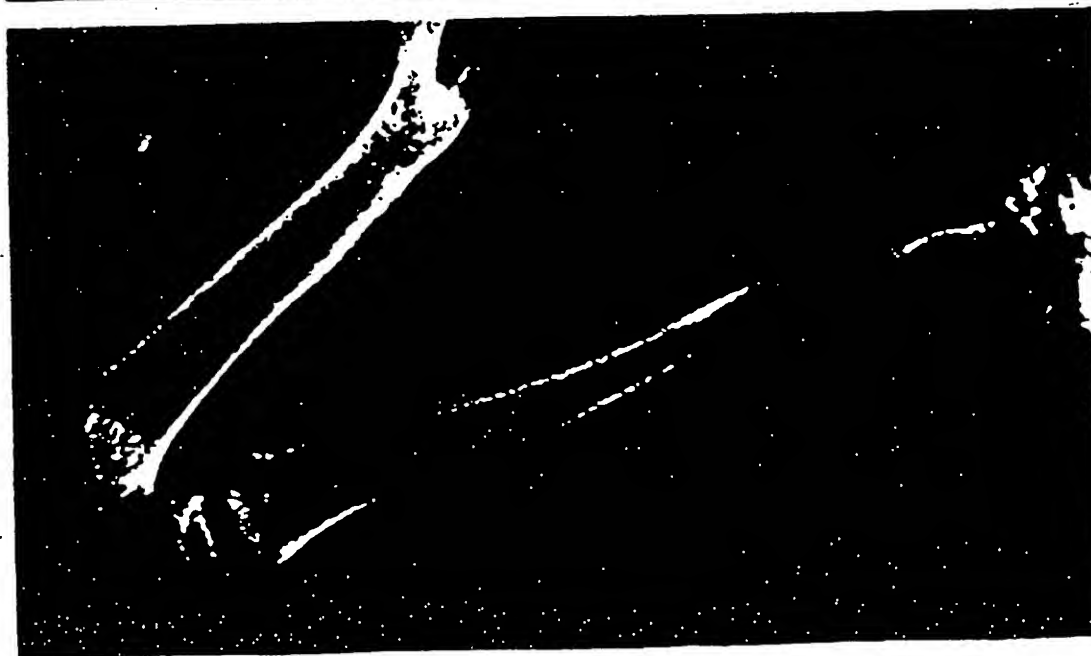
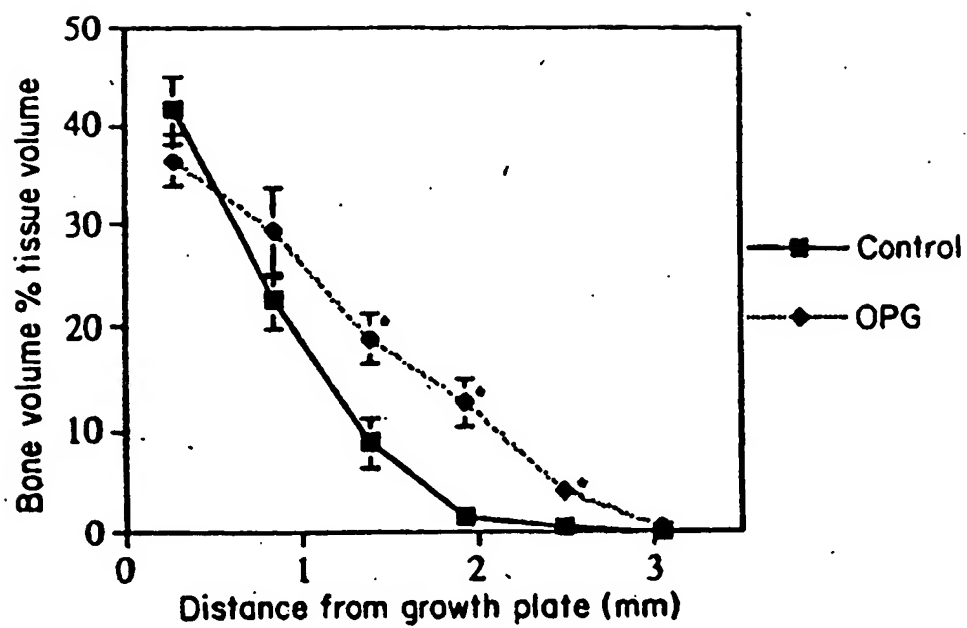




FIG.25



\* Different to control  $p < 0.01$



FIG.26A



FIG.26.B





FIG.27

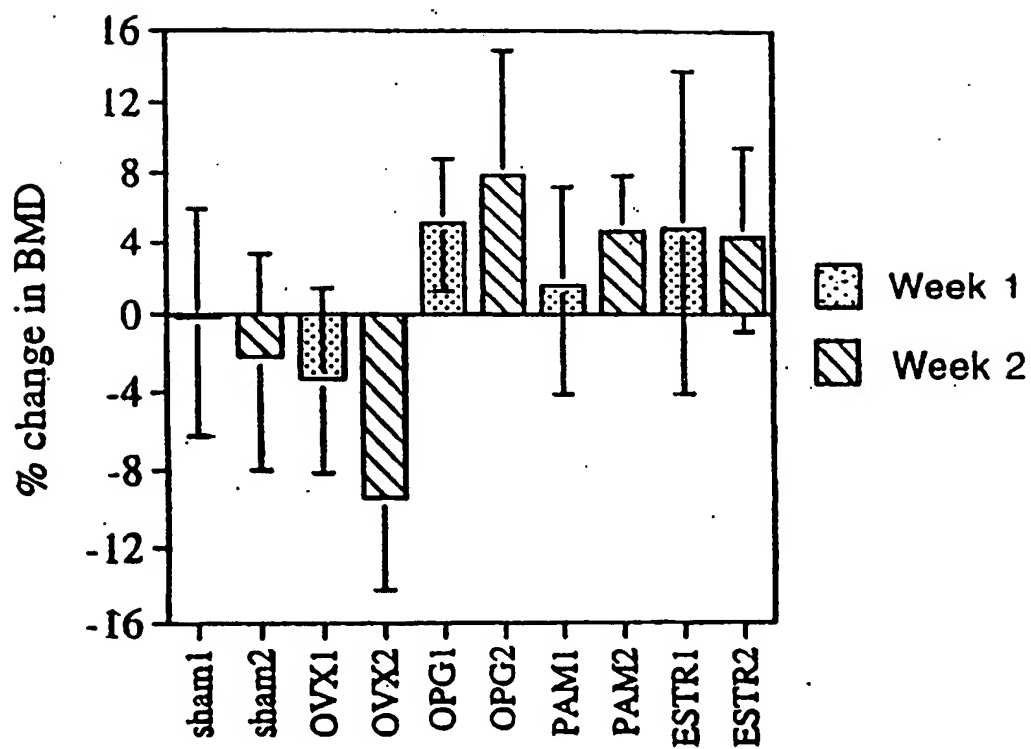
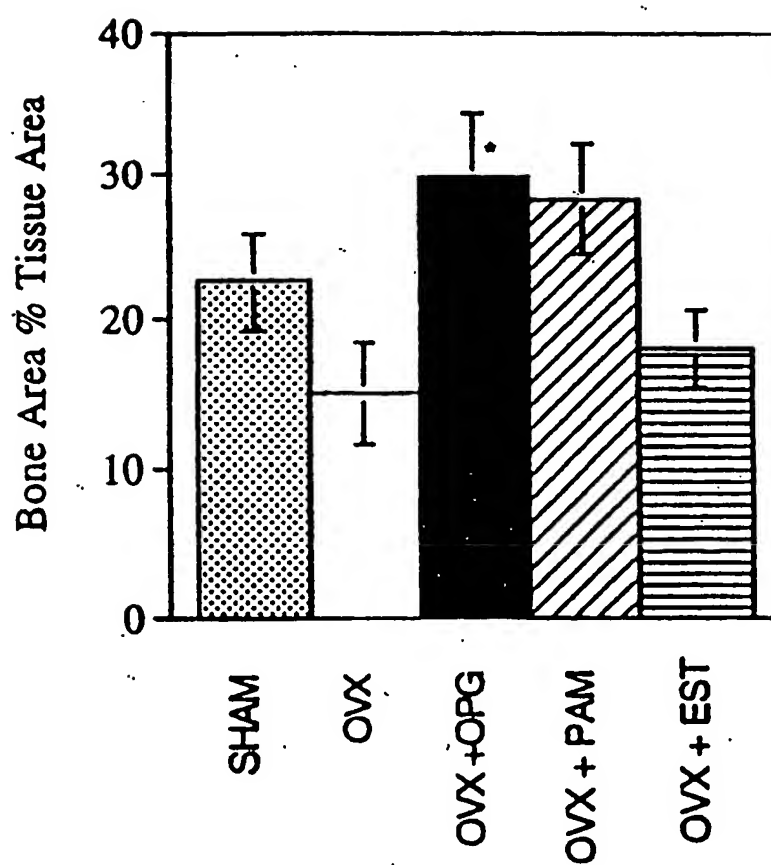




FIG.28



\* Different to OVX  $p < 0.05$



Dr III

1 CATGGGAAATGTCAGAGTGGAGAACCACACCGAGTGCCACTGCAGCACTTGTATTATCA  
GTACCCCTTTACAGTCTCACCTCTTGGTGTGGCTCACGGTGACGTCGTGAACAATAATAGT  
61 CAAATCTAATAGTTTGCAGTGGCCCTTGCTGATGATGGTGACTTGCTCAAAGGAAAA  
GTTTAGGATTATCAAACGTCACCCGGAACGACTACTACCGACTGAACGAGTTTCTCTTT  
121 TTAATTTGTCCAGTGTCTATGGCTTTGTGAGATAAAACCCCTCTTTCTTGCCATACCA  
AATTAACAGGTACAGATACCGAAACACTCTATTTTGGGAGGAAAAGGAACGGTATGGT  
181 TTTTAACTGCTTTGAGAATATATCTGAGCTTTATTGCTTTTCTCTTATCTACAATA  
AAAAATTGGACGAACTCTTATATGACGTCGAAATAACGAAAAGAGGAATAGGATGTTAT  
241 TAATCAGTAGTCTTGATCTTTTCATTGGAATGAAATATGGCATTAGCATGACCATAAA  
ATTAGTCATCAGAACTAGAAAAGTAAACCTTACTTTATACCGTAAATCGTACTGGTATTT  
301 AAGCTGATTCACCTGGAATAAAGTCTTTTAAATCATCACTCTATCACTGAATTCTAATT  
TTCCACTAAGGTGACCTTTATTTTCAGAAAAATTTAGTAGTGAGATAGTGACTTAAGATTAA  
361 TTTTCTGAAAAGTTTCAAGCCAGTTACTTTTGATAGGATTAAACGGAAGGAGTGAGCCAG  
AAAAGACTTTTCAAAGTTCGGTCAATGAAAACATCTCTAATTGCTTCCCTCACTCGGTC  
Xcrl  
421 TGGGTGAGGTGGTTCCTCATGTAGTCAATGGCCTAATCTGGAGAACTTATTCTAACCA  
ACCCACTCCACCAAGGGTACATCAGTTACCGGATTATGACCTCTTAGAATAAGATTGGT  
481 AGCCTTCAGAGCAAGCTGTGAGCCCTCAGACAGTGGGTACTCATGAGACAGTCCATT  
TCGGAAGGTCTCGTTTCGACACTCGGGGAGTCTGTACCCGATGAGTACTCTGTCAGGTAA  
541 GCGGTAAAGGAAGAAAATATACTTCTATTCTATTTCATTTCACATTGTCTTTAGATGC  
CCCCATTTCTCTTTTATATTGAAGATAAAGATAAGTAAACGTTGAACAGAAATCTACG  
601 CCATTTGGGTGAGTTTATAGAAGTACAGTACATTAAAAATAGAAGTATAATAGATA  
GGTAAACCACTCAAAATATCTTCATGTGCATGTAATTTTTTATCTTGACTATTATCTAT  
661 AGGCTTTAAAAAACTTCATTTCATCCAGTTTGTCAAGATTCCATTTCAAAGTAAAAAA  
TCCGAAATTTTTTTGAAGTAAGTAGTGGTCAAACAGTTCTAAGGTAAAGTTTCACTTTTT  
721 CCAATTTCAACGGGTGGTAAACACAGCAGATGGCAGGGTAAAAAATTAAGTGAGTGC  
GGTTAAAGATTGCCCAACCAATTTGTGTCTGTACCGTCCCACTTTTAAATTCACTCAGG  
781 ATGTACCTTTAAAGAAAACACTGAAATGCACACACATTACTTAACCTGCTCATTATTAT  
TACATGGAATTTCTTTGTGACTTTACGTGTGTGAATGAATTGGACGAGTAAGTAAATA  
841 TTACATATAGTCTTGGGTGTACAAAAATTTAGAAATAAATACATATGGGGCGGGGCCCTA  
AATGTATATCAGAACCCACATGTTTTAAATCTTTATTTATGTATACCCCGCCCGGGAAT  
901 GCTGCACAAATAGGATGCGCGCGGGCCCTGGTAGGGCGGAGCCTTAGCTGCACAAATA  
CGACGTGTTATCTACGCCCGCCCGGGAACCATCCCGCCTCGGAATCGACGTGTTTTAT  
961 GGATGCGCGCGGGCCCTTGGTGGGGCGGGCCCTAAGCTGCCAAGTGGTACACAGCTCA  
CCTACGCCCGCCCGGGAACCATCCCGCCTCGGAATCGACGTGTTTTAT  
1021 GGGCTGCGATTTCGCGCCAAACTTGACGGCAATCCTAGCTGAAGGCTGGTAGGATTTTA  
CCCGACGCTAAAGCGCGGTTTGAAGTGGCGTTAGGATGCGCACTTCGACCATCTTAAAT



Figure 29B

TCCCCGCTGCCATCATGTTTCGACCATTTGAAGTGCATCGTCGCCGTCTCCCAAAATATGG  
1081 .....+ 1140  
AGGGCCGACGGTAGTACCAAGCTGGTAACTTGACGTAGCAGCGCCACAGGGTTTATACC  
GGATTGGCAAGAACGGAGACCTACCTGGCCTCCGCTCAGGAACGAGTTCAAGTACTTCC  
1141 .....+ 1200  
CCTAACCGTTCTTGCCCTCTGGATGGGACCGGAGCGAGTCCTTGCTCAAGTTCATGAAGG  
AAAGAATGACCACAACCTCTTCAGTGGGAAGGTAACAGAATCTGGTGATTATGGGTAGGA  
1201 .....+ 1260  
TTTCTTACTGGTGTGGAGAAGTCACCTTCCATTGTCTTAGACCACTAATACCCATCCT  
AAACCTGGTTCTCCATTCTCTGAGAAGAATCGACCTTTAAAGGACAGAATTAATATAGTTC  
1261 .....+ 1320  
TTTGGACCAAGAGGTAAGGACTCTTCTTAGCTGGAATTTCTGTCTTAATTATATCAAG  
SacI BstXI  
TCAGTAGAGAACTCAAAGAACCACCGAGGAGCTCATTTTCTTGCCAAAAGTTGGATG  
1321 .....+ 1380  
AGTCATCTCTTGAGTTCTTGCTGGTGCTCCTCGAGTAAAAGAACGGTTTCAAACCTAC  
AflIII  
ATGCCTTAAGACTTATTGAACAACCGGAATTGGCAAGTAAAGTAGACATGGTTGGATAG  
1381 .....+ 1440  
TACCGAATTCTGAATAACTTGTGGCCTTAACCGTTCATTTCATCTGTACCAACCTATC  
TCGGAGGCAGTTCTGTTTACCAGGAAGCCATGAATCAACCGGCCACCTCAGACTCTTTG  
1441 .....+ 1500  
AGCCTCCGTCAGACAAATGGTCTTCCGTAAGTCTAGTTGGTCCGTCGAGTCTGAGAAAC  
TGACAAGGATCATGCAGGAATTTGAAAGTGACACGTTTTTCCAGAAATGATTGGGGA  
1501 .....+ 1560  
ACTGTTCTAGTAGTCCTTAAACTTTCAGTGTGCAAAAAGGGTCTTAACTAAACCCCT  
AATATAAACTTCTCCAGAATACCCAGCGCTCCTCTCTGAGGTCCAGGAGGAAAAAGGCA  
1561 .....+ 1620  
TTATATTTGAAGAGGGTCTTATGGGTCCGAGGAGAGACTCCAGGTCTCTTTTCCGT  
TCAAGTATAAGTTTGAAGTCTACGAGAAGAAAGACTAACAGGAAGATGCTTCAAGTTCT  
1621 .....+ 1680  
AGTTCATATTCAAACCTCAGATGCTCTTCTTCTGATTGTCCTTCTACGAAAGTTCAAGA  
BglII  
CTGCTCCCTCTCTAAAGCTATGCAATTTTATAAGACCATGGGACTTTTGTGGCTTTAGA  
1681 .....+ 1740  
GACGAGGGGAGGATTTCGATACGTAATAATATTCTGGTACCCTGAAAACGACCGAAATCT  
TCTGAAACACTGAAATGTCTGCTTCTCATCTTCAGTGAGATTCCAAGGATAGTACAGT  
1741 .....+ 1800  
AGACTTTGTGACTTTAACAGACGAAGAGTAGAAGTCACCTAAGGTTTCTATCATGTCA  
GACAGAACAAGATAGCCACTCTCTACAAAAAAGAAAGAAAAAAGTAAGTAATAGCAA  
1801 .....+ 1860  
CTGTCTTGTCTTATCCGTGAGAGATGTTTTTTTCTTCTTTTGTGATTCAATTATCGTT  
GCATAATAGCTACTGTTAAGAACTCAGAGATAATGAATTGAGAAATGATATGCTTGAAA  
1861 .....+ 1920  
CGTATTATCGATGACAAATCTTGAGTCTCTATTACTTAACTCTTACCTATGACGAACCTT  
TGAAAATTTAATAAGTTAGAACTAACTTTATAAAAAAATAAAAAATGAGCATTAAAAA  
1921 .....+ 1980  
ACTTTTAAATTATTCAATCTTTGATTTGAAATATTTTATTTTACTCGTAATTTTTT  
NheI  
AAAAAAAAAAAAAAAAAAAAACCCCCCCCCCCCCCTGCAGCCAAGCTAGCTTGGAAATC  
1981 .....+ 2040  
TTTTTTTTTTTTTTTTTTTGGGGGGGGGGGGGGGACGTCGGTTCGATCGAACCTTAG  
BspLU111  
ACGGGATAACGCAGGAAGAACATGTGAGCAAAAGCCAGCAAAAGCCAGCAACCGTAA



[illegible]



Figure 29D

CGTTGTTGCCATTGCTGCAGGCATCGTGGTGTACCGCTCGTCGTTTGGTATGGCTTCATT  
3181 ..... 3240  
GCAACAACGGTAACGACGTCCGTAGCACACAGTCCGAGCAGCAACCATACCGAAGTAA  
CAGCTCCGGTTCCTAACGATCAAGGCGAGTTACATGATCCCCATGTTGTGCAAAAAAGC  
3241 ..... 3300  
GTCGAGGCCAAGGGTTGCTAGTTCGGCTCAATGTACTAGGGGGTACAACACGTTTTTTTCG

PvuI      EaeI  
         GdIII

GGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAAGTAAGTTGGCCCGCAGTGTATCACT  
3301 ..... 3360  
CCAATCGAGGAAGCCAGGAGGCTAGCAACAGTCTTCATTCAACGGCGTCACAATAGTGA  
CATGGTTATGGCAGCACTGCATAATTCTTACTGTATGCCATCCGTAAGATGCTTTTC  
3361 ..... 3420  
GTACCAATACCGTCGTGACGTATTAAAGAGAATGACAGTACGGTAGGCATTCTACGAAAAG

BclI

TGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGCCGGCAGCCGAGTTG  
3421 ..... 3480  
ACACTGACCACTCATGAGTTGGTTCAAGTAACTCTTATCACATACGCCCGTGGCTCAAC  
CTCTTGGCCCGCGTCAACACGGGATAATACCGGCCACATAGCAGAACTTTAAAAGTGCT  
3481 ..... 3540  
GAGAACGGGCGCGAGTTGTGCCCTATTATGGCCGGTGTATCGTCTGAAATTTTCACGA  
CATCATTGGAACCGTCTCTCGGGCGGAACTCTCAAGGATCTTACCGCTGTTGAGATC  
3541 ..... 3600  
GTAGTAACCTTTTCAAGAAGCCCGCTTTTGAGAGTTCTAGAATGGCGACAACCTCTAG  
CAGTTCGATGTAACCACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTCACCAG  
3601 ..... 3660  
GTCAAGCTACATTGGGTGAGCAGTGGGTTGACTAGAAAGTCGTAGAAAATGAAAGTCGTC  
CGTTTCTGGGTGAGCAAAAACAGGAACGCAAAATGCCGCAAAAAGGGGAATAAGGGCGAC  
3661 ..... 3720  
GCAAGACCCACTCGTTTTTGTCTTCCGTTTTACGGCGTTTTTCCCTTATTCGGCTG

SspI

ACGGAAATGTTGAATACTCATACTCTTCCTTTTCAATATTATTGAAGCATTATCAGGG  
3721 ..... 3780  
TGCCCTTACAACCTATGAGTATGAGAAGGAAAAGTTATAATAACTTCGTAATAGTCCC  
TTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAACAAATAGCGGT  
3781 ..... 3840  
AATAACAGAGTACTCGCCTATGTATAAACTTACATAAATCTTTTTATTGTTTATCCCA  
TCCCGGCACATTTCCCGGAAAAGTGCCACCTGACGTCTAAGAAACATTATTATCATGAC  
3841 ..... 3900  
AGCGCGGTGTAAAGCGGCTTTTACGGTGGACTGCAGATTCTTTGGTAATAATAGTACTG  
ATTAACTATAAAAATAGCGGTATCAGGAGCCCTTTTCGTCTTCAAGAAATTCCTGTGGA  
3901 ..... 3960  
TAATTGGATATTTTATCCGATAGTGCTCCCGGAAAGCAGAGTTCTTAAGGACACCT  
ATGTGTGTCAGTTAGGGTGTGAAAGTCCCGAGGCTCCCGAGCAGGAGATGCAAA  
3961 ..... 4020  
TACACACAGTCAATCCACACCTTTACGGGTCGAGGGTCTCGTCTTCATACGTTT  
GCATGCATCTCAATTAGTCAGCAACAGGTGTGGAAAGTCCCGAGGCTCCCGAGCAGGCA  
4021 ..... 4080  
CGTACGTAGAGTTAATCAGTCGTGGTCCACACCTTTACGGGTCGAGGGGTGTCGGT  
GAAGTATGCAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCTAACTCCGC  
4081 ..... 4140  
CTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTGGTATCAGGCGGGGATTGAGGCG  
CCATCCCGCCCTAACTCCCGCCAGTTCGGCCCATTTCCCGCCCATGCGCTGACTAATTT  
4141 ..... 4200  
GGTAGGGCGGGATTGAGGCGGGTCAAGGCGGGTAAGAGCGGGGTACCGACTGATTAA



Figure 29E

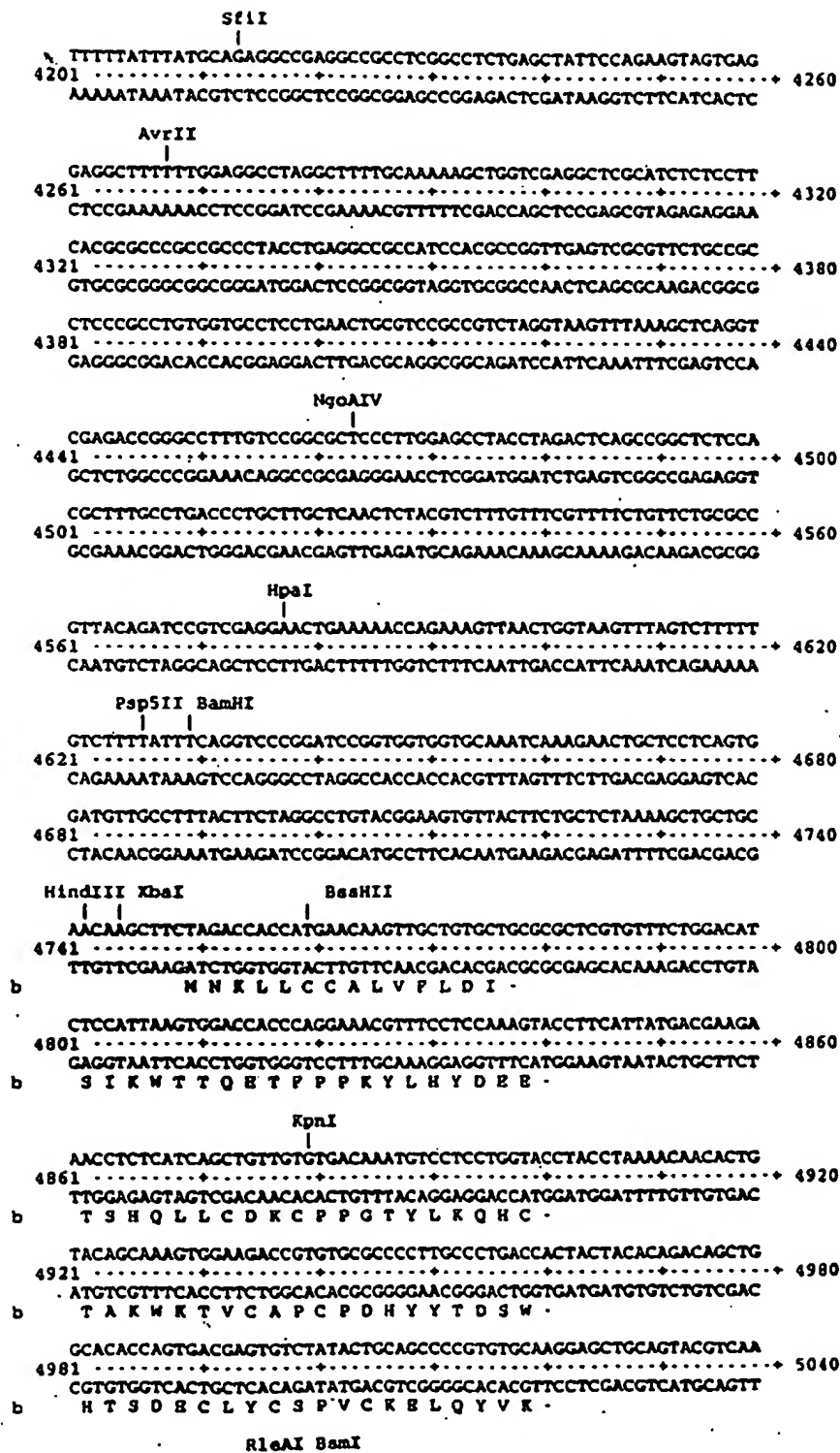




Figure 29F

GCAGGAGTGC AATCGCACCCACAACCGCGTGTGCGAATGCAAGGAAGGGCGCTACCTTGA  
5041 ..... 5100  
b CGTCCTCAGCTTAGCGTGGGTGTGCGCCACACGCTTACGTTCTCCCGGATGGAAC  
Q E C N R T H N R V C E C K E G R Y L E .

GATAGAGTTCTGCTTGAACATAGGAGCTGCCCTCCTGGATTGGAGTGGTCAAGCTGG  
5101 ..... 5160  
b CTATCTCAAGACGAACTTTGTATCTCGACGGGAGGACCTAAACCTCACCACGTTCCGACC  
I E F C L K H R S C P P G F G V V Q A G .

BsmBI  
AACCCAGAGCGAAATACAGTTTGC AAAAGATGTCAGATGGGTCTTCTCAAATGAGAC  
5161 ..... 5220  
b TTGGGGTCTCGCTTTATGTCAAACGTTTCTACAGGCTACCCAAGAAGATTACTCTG  
T P E R N T V C K R C P D G F P S N E T .

GTCATCTAAAGCACCTGTAGAAAACACAAAATTGCAGTGTCTTTGGTCTCCTGCTAAC  
5221 ..... 5280  
b CAGTAGATTTCTGCGGACATCTTTGTGTGTTTAACGTCACAGAAACCAGAGGAGATTG  
S S K A P C R K H T N C S V P G L L L T .

BspEI  
TCAGAAAGGAAATGCAACACACGACATATGTTCCGGAACAGTGAATCAACTCAAAA  
5281 ..... 5340  
b AGTCTTTCTCTTACGTTGTGTGCTGTGTATACAAGGCCTTTGTCACTTAGTTGAGTTT  
Q K G N A T H D N I C S G N S E S T Q K .

SalI BmgI  
AGTCGACAAAACCTCACACATGCCACCGTGCCACGACCTGAACTCCTGGGGGACCGTC  
5341 ..... 5400  
b TCAGCTGTTTTGAGTGTGTACGGGTGGCAGCGGTCTGGACTTGAGGACCCCTCGGCAG  
V D K T H T C P P C P A P E L L G G P S .

AGTCTTCTCTTCCCCCAAAACCAAGGACACCTCATGATCTCCCGGACCCCTGAGGT  
5401 ..... 5460  
b TCAGAAGGAGAAGGGGGTTTGGGTCTCTGTGGGAGTACTAGAGGGCTGGGGACTCCA  
V P L F P P K P K D T L M I S R T P E V .

BtrI  
CACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGT  
5461 ..... 5520  
b GTGTACGCACACCACTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCA  
T C V V V D V S H E D P E V K P N W Y V .

SacII  
CGACGGCGTGGAGGTGCATAATGCCAAGACAAGCCGGGGAGGAGCAGTACAACAGCAC  
5521 ..... 5580  
b CCTGCCGCACCTCCAGGTATTACGGTTCTGTTCCGGCCCTCTCTGTCATGTTGTCTGTG  
D G V E V H N A K T K P R E E Q Y N S T .

GTACCGTGTGGTCAAGCTCTCACCGTCTCCACGAGGACTGGCTGAATGGCAAGGAGTA  
5581 ..... 5640  
b CATGGCACACCACTCCAGGAGTGGCAGGACGTGCTGACCGACTTACCGTCTCTCAT  
Y R V V S V L T V L H Q D W L N G K E Y .

CAAGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCATCGAGAAAACCATCTCCAAGC  
5641 ..... 5700  
b GTTCACGTTCCAGAGGTTGTTTCGGGAGGGTCCGGGTACCTTTTGGTAGAGGTTTCG  
K C K V S N K A L P A P I E K T I S K A .

SmaI  
CAAAGGGCAGCCCCGAGAACCACAGGTGTACACCTGCCCCCATCCCGGGATGAGCTGAC  
5701 ..... 5760  
b GTTCCCGTCCGGGCTCTTGGTGTCCACATGTGGGACGGGGTACGGCCCTACTCGACTG  
K G Q P R E P Q V Y T L P P S R D E L T .

CAAGAACCAGGTACGCTGACCTGCTGTCAAAGGCTTCTATCCAGCGACATCGCCGT  
5761 ..... 5820  
b GTTCTTGGTCCAGTCCGACTCGACGGACCAAGTTTCCGAAGATAGGGTCCGTGTACGGCA



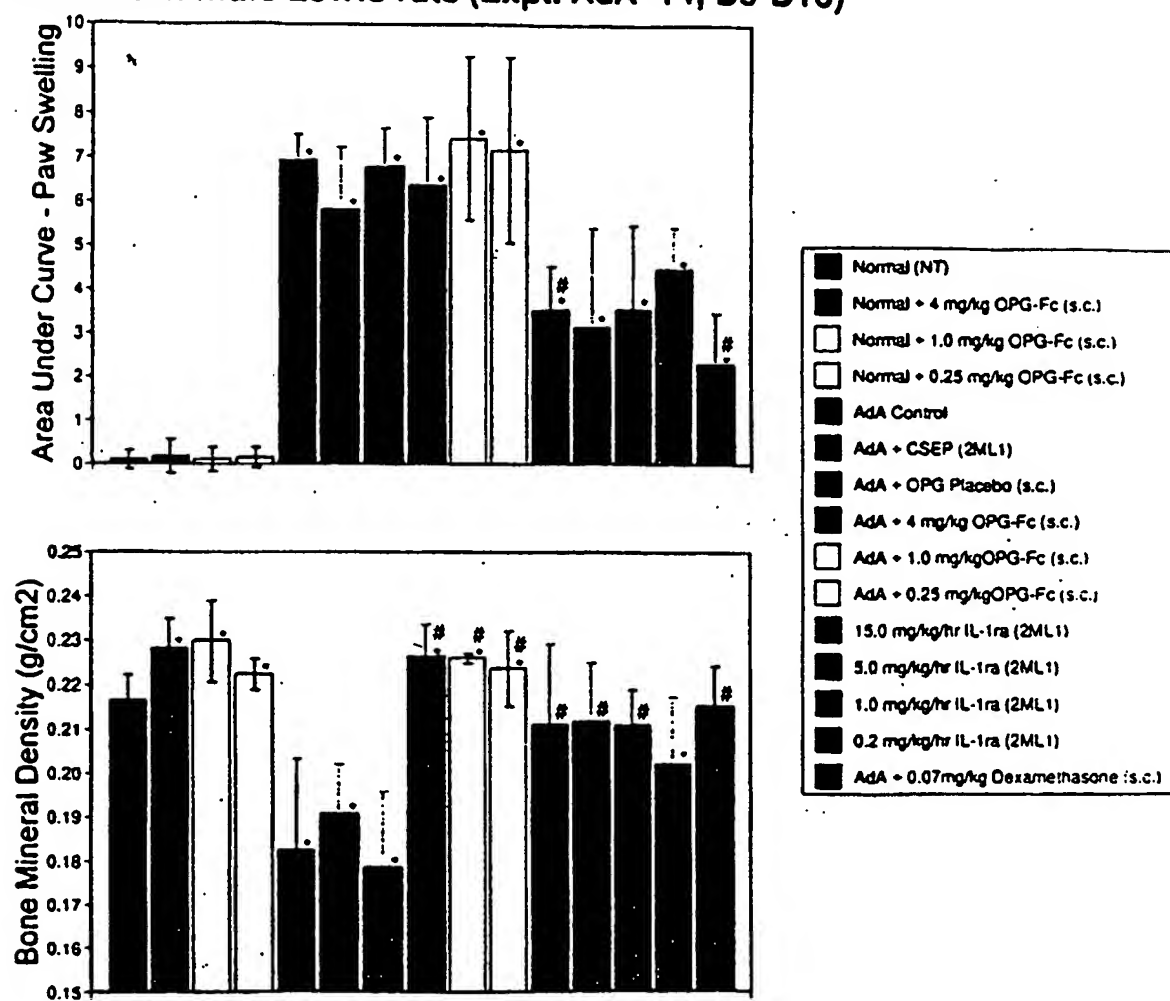
Figure 29G

b K N Q V S L T C L V K G F Y P S D I A V -  
CGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACAGACCACGCCTCCCGTCTCGA  
5881 ..... 5880  
CCTCACCCCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGTCGGAGGGCAGGACCT  
b E W E S N G Q P E N N Y K T T P P V L D -  
AarI  
CTCCGACGGCTCCTTCTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGCCAGCA  
5881 ..... 5940  
GAGGCTGCCGAGGAAGAAGGAGATGTCGTTCCAGTGGCACCTGTTCTCGTCCACCGTCGT  
b' S D G S P F L Y S K L T V D K S R W Q Q -  
SapI  
GGGGAACGCTCTTCTCATGCTCCGTGATGATGAGGCTCTGCACAACCACTACACGCAGAA  
5941 ..... 6000  
CCCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGCTGATGTCCGCTCT  
b G N V F S C S V M H B A L H N H Y T Q K -  
GAGCCTCTCCCTGTCTCCGGGTAAATGATAACTCGAC  
6001 ..... 6037  
CTCGGAGAGCGGACAGAGGCCCATTTACTATTGAGCTG  
b S L S L S P G K \* \*



Figure 30A

### Effects of OPG-Fc during the course of adjuvant arthritis in male Lewis rats (Expt. AdA- 14, D9-D16)



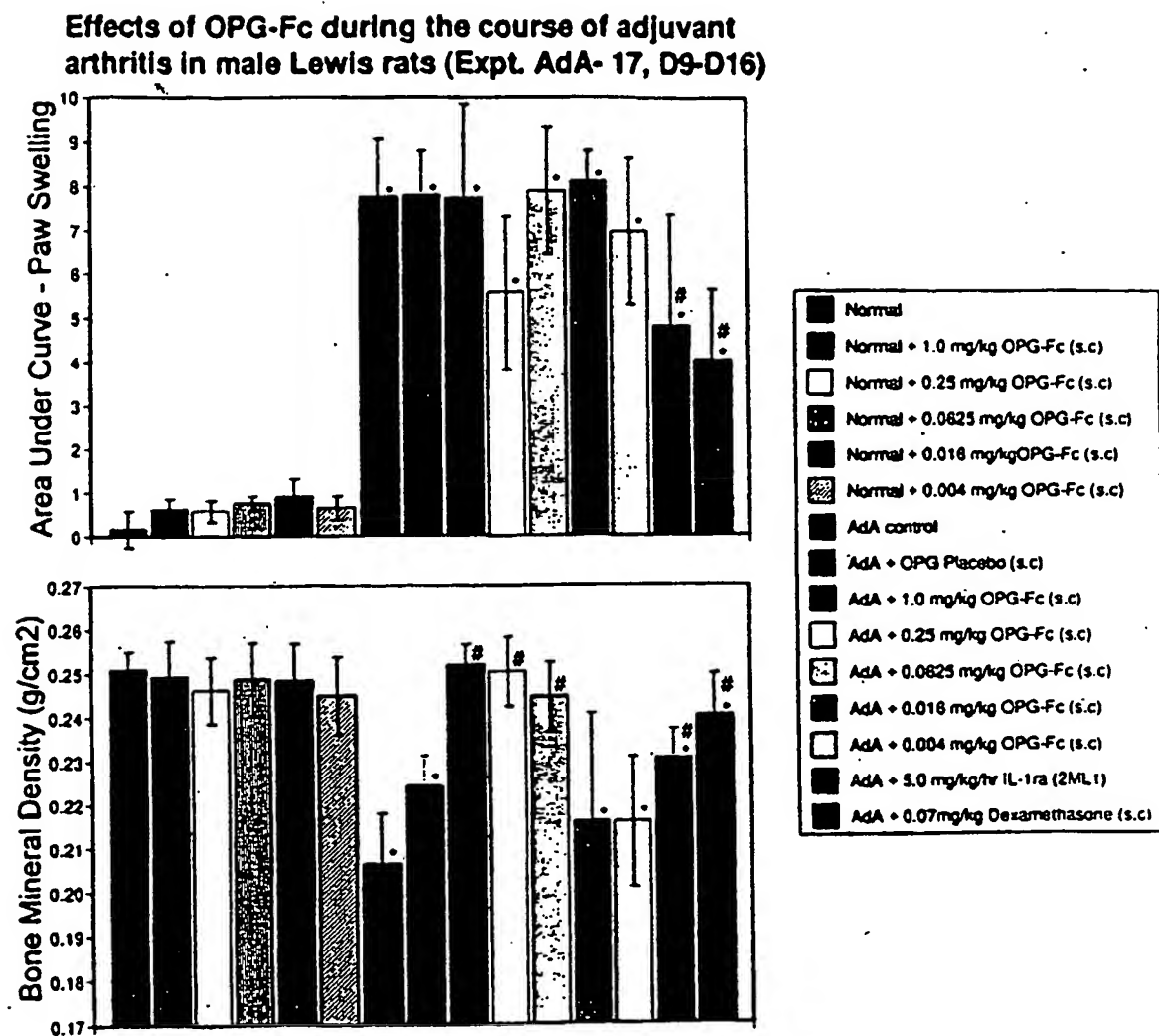
Paws from rats with adjuvant arthritis induced by 0.5mg mycobacteria in oil were analyzed by DEXA for BMD. Evaluation of BMD, a 29mm X 25mm box was centered at the calcaneus (expt AdA-14 2/99, Amgen nb#22957 p47-49).

\* compared to normal, # compared to vehicle

P < 0.05 Mann-Whitney U test



Figure 30B



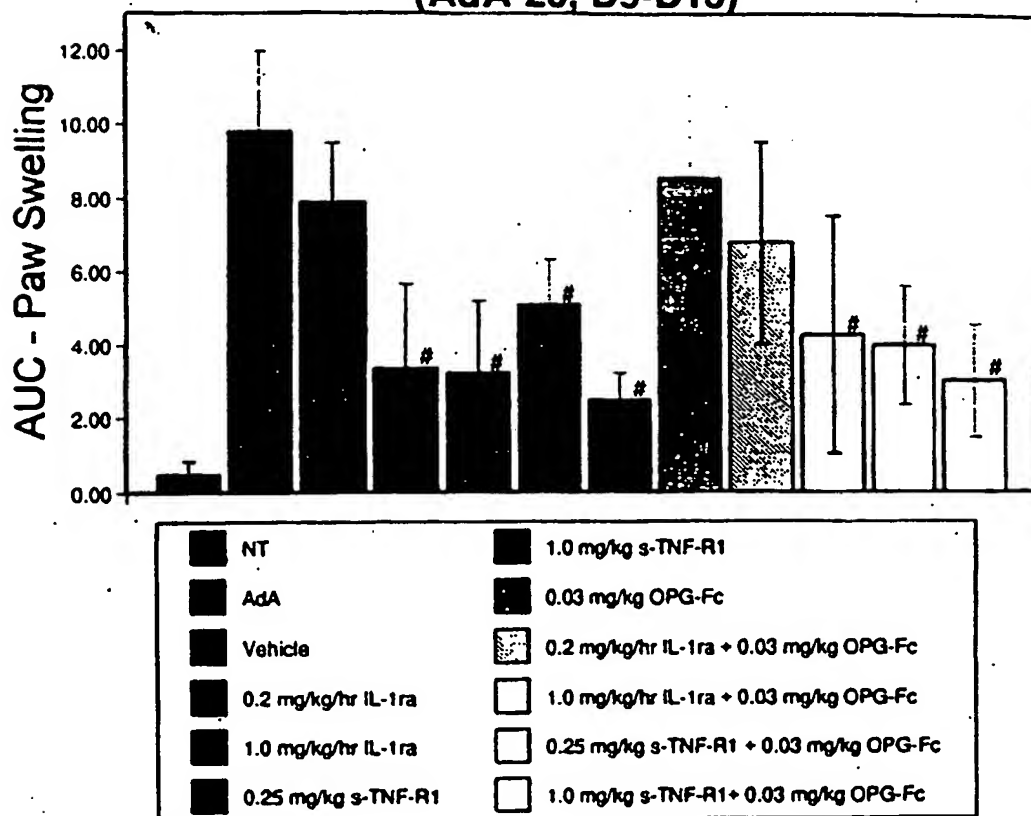
Paws from rats with adjuvant arthritis induced by 0.5mg mycobacteria in oil were analyzed by DEXA for BMD. Evaluation of BMD, a 29mm X 25mm box was centered at the calcaneus (expt AdA -17 3/99, Amgen nb#22957 p62-65).

\* compared to normal, # compared to vehicle  
P < 0.05 Mann-Whitney U test



Figure 31A

**Combination treatment with OPG-Fc and IL-1ra or s-TNF-R1 on adjuvant arthritis in male Lewis rats (AdA-20, D9-D15)**



Paws from rats with adjuvant arthritis induced by 0.5mg mycobacteria in oil were analyzed by DEXA for BMD. (expt AdA-20 5/99, Amgen nb#22957 p84).

\* compared to normal, # compared to vehicle

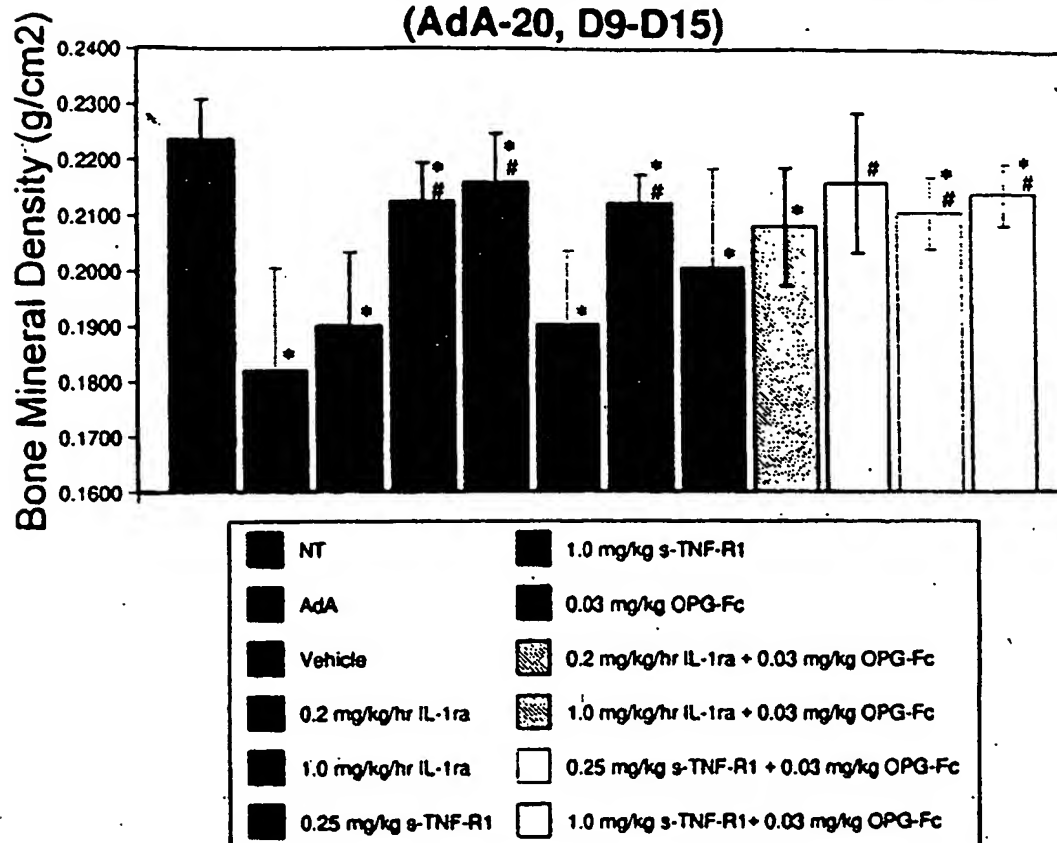
P < 0.05 Mann-Whitney U test

All groups are significant vs normal



Figure 31B

**Combination treatment with OPG-Fc and IL-1ra or s-TNF-R1 on adjuvant arthritis in male Lewis rats (AdA-20, D9-D15)**



Paws from rats with adjuvant arthritis induced by 0.5mg mycobacteria in oil were analyzed by OEXA for BMD. Evaluation of BMD, a 29mm X 25mm was centered at the tibiotarsal region. (expt AdA-20 5/99, Amgen nb#22957 p88).

\* compared to normal, # compared to vehicle

P < 0.05 Mann-Whitney U test.



## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: Amgen Inc.

(ii) TITLE OF INVENTION: OSTEOPROTEGERIN

(iii) NUMBER OF SEQUENCES: 168

## (iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Amgen Inc.
- (B) STREET: 1840 Dehavilland Drive
- (C) CITY: Thousand Oaks
- (D) STATE: California
- (E) COUNTRY: United States
- (F) ZIP: 91320

## (v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

## (vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:

## (viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Winter, Robert B.
- (C) REFERENCE/DOCKET NUMBER: A-378-CIP2

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA



2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAAGGAAGGA AAAAAGCGGC CGCTACANNN NNNNNT

36

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TCGACCCACG CGTCCG

16

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGGTGCGCAG GC

12

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TGTAACACGA CGGCCAGT

18



3

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CAGGAAACAG CTATGACC

18

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CAATTAACCC TCACTAAAGG

20

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCATTATGAC CCAGAAACCG GAC

23

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:



4

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AGGTAGCGCC CTCCTCACA TTC

23

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GACTAGTCCC ACAATGAACA AGTGGCTGTG

30

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATAAGAATGC GGCCGCTAAA CTATGAAACA GCCCAGTGAC CATTC

45

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCCTCTAGAA AGAGCTGGGA C

21

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGCCGTGTTT CATTATGAG C

21

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATCAAAGGCA GGGCATACTT CCTG

24

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GTTGCACTCC TGTTCACGG TCTG

24

(2) INFORMATION FOR SEQ ID NO:15:



6

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CAAGACACCT TGAAGGGCCT GATG

24

## (2) INFORMATION FOR SEQ ID NO:16:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TAACTTTTAC AGAAGAGCAT CAGC

24

## (2) INFORMATION FOR SEQ ID NO:17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGCGCGGCCG CATGAACAAG TGGCTGTGCT GCG

33

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear



7

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AGCTCTAGAG AACAGCCCA GTGACCATTC C

31

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GTGAAGCTGT GCAAGAACCT GATG

24

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATCAAAGGCA GGGCATACTT CCTG

24

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CAGATCCTGA AGCTGCTCAG TTTG

24

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

AGCGCGGCCG CGGGGACCAC AATGAACAAG TTG

33

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AGCTCTAGAA TTGTGAGGAA ACAGCTCAAT GGC

33

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:



ATAGCGGCCG CTGAGCCCAA ATCTGTGAC AAAACTCAC

39

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TCTAGAGTCG ACTTATCATT TACCCGGAGA CAGGGAGAGG CTCTT

45

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CCTCTGAGCT CAAGCTCCG AGGACCACAA TGAACAAG

38

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CCTCTGCGGC CGCTAAGCAG CTTATTTTCA CGGATTGAAC CTG

43

(2) INFORMATION FOR SEQ ID NO:28:



10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CCTCTGAGCT CAAGCTTCCG AGGACCACAA TGAACAAG

38

## (2) INFORMATION FOR SEQ ID NO:29:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TCCGTAAGAA ACAGCCCACT GACC

24

## (2) INFORMATION FOR SEQ ID NO:30:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CCTCTGCGGC CGCTGTTGCA TTTCCTTCT G

31

## (2) INFORMATION FOR SEQ ID NO:31:

## (i) SEQUENCE CHARACTERISTICS:



11

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Glu Thr Leu Pro Pro Lys Tyr Leu His Tyr Asp Pro Glu Thr Gly His  
1           5           10           15

Gln Leu Leu

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TCCCTTGCCC TGACCACTCT T

21

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CCTCTGCGGC CGCACACAG TTGTCATGTG TTGC

34

(2) INFORMATION FOR SEQ ID NO:34:



12

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TCCCTTGCCC TGACCACTCT T

21

## (2) INFORMATION FOR SEQ ID NO:35:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CCTCTGCGGC CGCCTTTTGC GTGGCTTCTC TGTT

34

## (2) INFORMATION FOR SEQ ID NO:36:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA.

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CCTCTGAGCT CAAGCTTGGT TTCCGGGGAC CACAATG

37

## (2) INFORMATION FOR SEQ ID NO:37:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs



13

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CCTCTGCCGC CGCTAAGCAG CTTATTTTCTA CTGAATGG

38

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CCTCTGAGCT CAAGCTTGGT TTCCGGGGAC CACAATG

37

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CCTCTGCCGC CGCCAGGGTA ACATCTATTC CAC

33

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single



14

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CCGAAGCTTC CACCATGAAC AAGTGGCTGT GCTGC

35

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CCTCTGTCGA CTATTATAAG CAGCTTATTT TCACGGATTG

40

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TCCCTTGCCC TGACCACTCT T

21

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA



15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CCTCTGTCGA CTTAACACAC GTTGTCATGT GTTGC

35

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

TCCCTTGCCC TGACCACTCT T

21

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CCTCTGTCGA CTTACTTTTG CGTGGCTTCT CTGTT

35

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1537 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA



16

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GTGAAGAGCG TGAAGAGCGG TTCCTCCTTT CAGCAAAAAA CCCCTCAAGA CCCGTTTAGA  
60

GGCCCCAAGG GGTATGCTA GTTATTGCTC AGCGGTGGCA GCAGCCAAC T CAGCTTCCTT  
120

TCGGGCTTTC TTCTTCTTCT TCTTCTTTCC GCGGATCCTC GAGTAAGCTT CCATGGTACC  
180

CTGCAGGTCG AACTAGTGA GCTCGAATTC CAACGCGTTA ACCATATGTT ATTCTCCTT  
240

TAATTAGTTA AAACAAATCT AGAATCAAAT CGATTAATCG ACTATAACAA ACCATTTTCT  
300

TGCGTAAACC TGTACGATCC TACAGGTACT TATGTAAAC AATTGTATTT CAAGCGATAT  
360

AATAGTGTGA CAAAAATCCA ATTTATTAGA ATCAAATGTC AATCTATTAC CGTTTTAATG  
420

ATATATAACA CGCAAACTT GCGACAAACA ATAGGTAAGG ATAAAGAGAT GGGTATGAAA  
480

GACATAATG CCGACGACAC TTACAGAATA ATTAATAAAA TTAAAGCCTG TAGAAGCAAT  
540

AATGATATTA ATCAATGCTT ATCTGATATG ACTAAATGG TACATTGTGA ATATTATTTA  
600

CTCGCGATCA TTTATCCTCA TTCTATGGTT AAATCTGATA TTTCAATTCT GGATAATTAC  
660

CCTAAAAAAT GGAGGCAATA TTATGATGAC GCTAATTTAA TAAATATGA TCCTATAGTA  
720

GATTATTCTA ACTCCAATCA TTCACCGATT AATTGGAATA TATTTGAAAA CAATGCTGTA  
780

AATAAAAAAT CTCCAAATGT AATTAAAGAA GCGAAATCAT CAGGTCTTAT CACTGGGTTT  
840

AGTTTCCCTA TTCATACTGC TAATAATGGC TTCGGAATGC TTAGTTTTGC ACATTCAGAG  
900

AAAGACAACT ATATAGATAG TTTATTTTGA CATGCGTGTA TGAACATACC ATTAATTGTT  
960

CCTTCTCTAG TTGATAATTA TCGAAAAATA AATATAGCAA ATAATAAATC AAACAACGAT  
1020



17

TTAACCAAAA GAGAAAAAGA ATGTTTAGCG TGGGCATGCG AAGGAAAAAG CTCTTGGGAT  
1080

ATTTCAAAAA TATTAGGCTG TAGTAAGCGC ACGGTCACCT TCCATTTAAC CAATGCGCAA  
1140

ATGAAACTCA ATACAACAAA CCGCTGCCAA AGTATTTCTA AAGCAATTTT AACAGGAGCA  
1200

ATTGATTGCC CATACTTTAA AAGTTAAGTA CGACGTCCAT ATTTGAATGT ATTTAGAAAA  
1260

ATAAACAAAA GAGTTTGTAG AAACGCAAAA AGGCCATCCG TCAGGATGGC CTTCTGCTTA  
1320

ATTTGATGCC TGGCAGTTTA TGGCGGGCGT CCTGCCCCGC ACCCTCCGGG CCGTTGCTTC  
1380

GCAACGTTCA AATCCGCTCC CGGCGGATTT GTCCTACTCA GGAGAGCGTT CACCGACAAA  
1440

CAACAGATAA AACGAAAGGC CCAGTCTTTC GACTGAGCCT TTCGTTTAT TTGATGCCTG  
1500

GCAGTTCCTT ACTCTCGCAT GGGGAGACCA TGCATAC 1537

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CCGGCGGACA TTTATCACAC AGCAGCTGAT GAGAAGTTTC TTCATCCA 48

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CGATTTGATT CTAGAAGGAG GAATAACATA TGGTTAACGC GTTGAATTC GGTAC  
55

## (2) INFORMATION FOR SEQ ID NO:49:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CGAATTCCAA CGCGTTAACC ATATGTTATT CCTCCTTCTA GAATCAAAT 49

## (2) INFORMATION FOR SEQ ID NO:50:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1546 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GCGTAACGTA TGCATGGTCT CCCCATGCGA GAGTAGGGAA CTGCCAGGCA TCAAATAAAA  
60

CGAAAGGCTC AGTCGAAAGA CTGGGCCTTT CGTTTTATCT GTTGTTTGTC GGTGAACGCT  
120

CTCCTGAGTA GGACAAATCC GCCGGGAGCG GATTGTAACG TTGCGAAGCA ACGGCCCGGA  
180

GGGTGGCGGG CAGGACGCCC GCCATAAACT GCCAGGCATC AAATTAAGCA GAAGGCCATC  
240



CTGACGGATG GCCTTTTTCG GTTTCTACAA ACTCTTTTGT TTATTTTCT AAATACATTC  
300

AAATATGGAC GTCGTACTTA ACTTTTAAAG TATGGGCAAT CAATTGCTCC TGTAAAATT  
360

GCTTTAGAAA TACTTTGGCA GCGGTTTGT GTATTGAGTT TCATTGCGC ATTGGTTAAA  
420

TGGAAAGTGA CCGTGCGCTT ACTACAGCCT AATATTTTGT AAATATCCCA AGAGCTTTT  
480

CCTTCGCATG CCCACGCTAA ACATTCTTTT TCTCTTTGG TTAAATCGTT GTTTGATTTA  
540

TTATTTGCTA TATTTATTTT TCGATAATTA TCAACTAGAG AAGGAACAAT TAATGGTATG  
600

TTCATACAG CATGTAAAA TAACTATCT ATATAGTTGT CTTTCTCTGA ATGTGCAAAA  
660

CTAAGCATTC CGAAGCCATT ATTAGCAGTA TGAATAGGGA AACTAAACCC AGTGATAAGA  
720

CCTGATGATT TCGCTTCTTT AATTACATTT GGAGATTTT TATTACAGC ATTGTTTCA  
780

AATATATTCC AATTAATCGG TGAATGATTG GAGTTAGAAT AATCTACTAT AGGATCATAT  
840

TTTATTAAAT TAGCGTCATC ATAATATTGC CTCCATTTT TAGGGTAATT ATCCAGAATT  
900

GAAATATCAG ATTTAACCAT AGAATGAGGA TAAATGATCG CGAGTAAATA ATATTCACAA  
960

TGTACCATTT TAGTCATATC AGATAAGCAT TGATTAATAT CATTATTGCT TCTACAGGCT  
1020

TTAATTTTAT TAATTATTCT GTAAGTGTG TCGGCATTTA TGTCTTTCAT ACCCATCTCT  
1080

TTATCCTTAC CTATTGTTT TCGCAAGTTT TCGGTGTTAT ATATCATTAA AACGGTAATA  
1140

GATTGACATT TGATTCTAAT AAATTGGATT TTTGTCACAC TATTATATCG CTTGAAATAC  
1200

AATTGTTTAA CATAAGTACC TGTAGGATCG TACAGGTTTA CGCAAGAAAA TGGTTTGTTA  
1260

TAGTCGATTA ATCGATTTGA TTCTAGATTT GTTTTAACTA ATTAAAGGAG GAATAACATA  
1320



20

TGGTTAACGC GTTGAATTC GAGCTCACTA GTGTCGACCT GCAGGGTACC ATGGAAGCTT  
1380

ACTCGAGGAT CCGCGGAAAG AAGAAGAAGA AGAAGAAAGC CCGAAAGGAA GCTGAGTTGG  
1440

CTGCTGCCAC CGCTGAGCAA TAACTAGCAT AACCCCTTGG GGCCTCTAAA CGGGTCTTGA  
1500

GGGGTTTTTT GCTGAAAGGA GGAACCGCTC TTCACGCTCT TCACGC 1546

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

TATGAAACAT CATCACCATC ACCATCATGC TAGCGTTAAC GCGTTGG 47

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

AATTCCAACG CGTTAAGCT AGCATGATGG TGATGGTGAT GATGTTTCA 49

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 base pairs
- (B) TYPE: nucleic acid



21

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CTAATTCGCG TCTCACCTAC CAAACAATGC CCCCTGCAA AAAATAAATT CATATAAAAA  
60

ACATACAGAT AACCATCTGC GGTGATAAAT TATCTCTGGC GGTGTTGACA TAAATACCAC  
120

TGGCGGTGAT ACTGAGCACA T 141

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CGATGTGCTC AGTATCACCG CCAGTGGTAT TTATGTCAAC ACCGCCAGAG ATAATTTATC  
60

ACCGCAGATG GTTATCTGTA TGTTTTTTAT ATGAATTTAT TTTTGCAGG GGGGCATTGT  
120

TTGGTAGGTG AGAGCGGAAT TAGACGT 147

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CGATTTGATT CTAGAAGGAG GAATAACATA TGGTTAACGC GTTGAATTC GGTAC  
55.

## (2) INFORMATION FOR SEQ ID NO:56:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CGAATTCCAA CGCGTTAACC ATATGTTATT CCTCCTTCTA GAATCAAAT 49.

## (2) INFORMATION FOR SEQ ID NO:57:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 668 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GTGAAGAGCG TGAAGAGCGG TTCCTCCTTT CAGCAAAAAA CCCCTCAAGA CCCGTTTAGA  
60.

GGCCCCAAGG GGTATGCTA GTTATTGCTC AGCGGTGGCA GCAGCCAACCT CAGCTTCCTT  
120

TCGGGCTTTC TTCTTCTTCT TCTTCTTCC GCGGATCCTC GAGTAAGCTT CCATGGTACC  
180

CTGCAGGTCG AACTAGTGA GCTCGAATTC CAACGCGTTA ACCATATGTT ATTCCTCCTT  
240



TAATTAGTTA ACTCAAATCT AGAATCAAAT CGATAAATTG TGAGCGCTCA CAATTGAGAA  
300

TATTAATCAA GAATTTTAGC ATTTGTCAAA TGAATTTTTT AAAAATTATG AGACGTCCAT  
360

ATTTGAATGT ATTTAGAAAA ATAAACAAAA GAGTTTGTAG AAACGCAAAA AGGCCATCCG  
420

TCAGGATGGC CTTCTGCTTA ATTTGATGCC TGGCAGTTTA TGGCGGGCGT CCTGCCCCGC  
480

ACCCTCCGGG CCGTTGCTTC GCAACGTTCA AATCCGCTCC CGGCGGATTT GTCCTACTCA  
540

GGAGAGCGTT CACCGACAAA CAACAGATAA AACGAAAGGC CCAGTCTTTC GACTGAGCCT  
600

TTCGTTTTAT TTGATGCCTG GCAGTTCCTT ACTCTCGCAT GGGGAGACCA TGCATACGTT  
660

ACGCACGT

668

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GCGTAACGTA TGCATGGTCT CCCCATGCGA GAGTAGGGAA CTGCCAGGCA TCAAATAAAA  
60

CGAAAGGCTC AGTCGAAAGA CTGGGCCTTT CGTTTTATCT GTTGTGTTGTC GGTGAACGCT  
120

CTCCTGAGTA GGACAAATCC GCCGGGAGCG GATTTGAACG TTGCGAAGCA ACGGCCCGGA  
180

GGGTGGCGGG CAGGACGCCC GCCATAAACT GCCAGGCATC AAATTAAGCA GAAGGGGCCT  
240

CCCACCGCCC GTCCTGCGGG CGGTATTGA CGGTCCGTAG TTTAATTCGT CTTGCCCATC  
300



24

CTGACGGATG GCCTTTTTCG GTTCTACAA ACTCTTTTGT TTATTTTCT AAATACATTC  
360

AAATATGGAC GTCTCATAAT TTTTAAAAA TTCATTGAC AAATGCTAAA ATTCTTGATT  
420

AATATTCTCA ATTGTGAGCG CTCACAATTT ATCGATTGA TTCTAGATTT GTTTTAACTA  
480

ATTAAAGGAG GAATAACATA TGGTTAACGC GTTGAATTC GAGCTACTA GTGTCGACCT  
540

GCAGGGTACC ATGGAAGCTT ACTCGAGGAT CCGCGGAAAG AAGAAGAAGA AGAAGAAAGC  
600

CCGAAAGGAA GCTGAGTTGG CTGCTGCCAC CGCTGAGCAA TAACTAGCAT AACCCCTTGG  
660

GGCCTCTAAA CGGGTCTTGA GGGGTTTTTT GCTGAAAGGA GGAACCGCTC TTCACGCTCT  
720

TCACGC

726

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:59:

TACGCACTGG ATCCTTATAA GCAGCTTATT TTTACTGATT GGAC

44

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear



25

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GTCCTCCTGG TACCTACCTA AAACAAC

27

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

TATGGATGAA GAAACTTCTC ATCAGCTGCT GTGTGATAAA TGTCCGCCGG GTACCCGGCG  
60

GACATTTATC ACACAGCAGC TGATGAGAAG TTTCTTCATC CA

102

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Met Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro  
1 5 10 15

Gly Thr Tyr

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 base pairs

(B) TYPE: nucleic acid



26

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

TATGGAAACT TTTCTCCAA AATATCTTCA TTATGATGAA GAACTTCTC ATCAGCTGCT  
60

GTGTGATAAA TGTCCGCCGG GTAC

84

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

CCGGCGGACA TTTATCACAC AGCAGCTGAT GAGAAGTTTC TTCATCATAA TGAAGATATT  
60

TTGGAGGAAA AGTTTCCA

78

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TACGCACTGG ATCCTTATAA GCAGCTTATT TTCACGGATT GAAC

44

(2) INFORMATION FOR SEQ ID NO:66:



27

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GTGCTCCTGG TACCTACCTA AACAGCACT GCACAGTG

38

## (2) INFORMATION FOR SEQ ID NO:67:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

TATGGAACT CTGCCTCAA AATACCTGCA TTACGATCCG GAACTGGTC ATCAGCTGCT  
60

GTGTGATAAA TGTGCTCCGG GTAC

84

## (2) INFORMATION FOR SEQ ID NO:68:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

CCGGAGCACA TTTATCACAC AGCAGCTGAT GACCAGTTTC CGGATCGTAA TGCAGGTATT  
60



28

TTGGAGGCAG AGTTTCCA

78

## (2) INFORMATION FOR SEQ ID NO:69:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

TATGGACCCA GAACTGGTC ATCAGCTGCT GTGTGATAAA TGTGCTCCGG GTAC  
54

## (2) INFORMATION FOR SEQ ID NO:70:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

CCGGAGCACA TTTATCACAC AGCAGCTGAT GACCAGTTTC TGGGTCCA

48

## (2) INFORMATION FOR SEQ ID NO:71:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:



29

TATGAAAGAA ACTCTGCCTC CAAAATACCT GCATTACGAT CCGGAAACTG GTCATCAGCT  
60

GCTGTGTGAT AAATGTGCTC CGGGTAC

87

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

CCGGAGCACA TTTATCACAC AGCAGCTGAT GACCAGTTTC CGGATCGTAA TGCAGGTATT  
60

TTGGAGGCAG AGTTTCTTTC A

81

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GTTCTCCTCA TATGAAACAT CATCACCATC ACCATCATGA AACTCTGCCT CAAAATACC  
60

TGCATTACGA T

71

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid



30

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GTTCTCCTCA TATGAAAGAA ACTCTGCCTC CAAAATACCT GCA

43

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

TACGCACTGG ATCCTTAATG ATGGTGATGG TGATGATGTA AGCAGCTTAT TTTCACGGAT  
60

TGAACCTGAT TCCCTA

76

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GTTCTCCTCA TATGAAATAC CTGCATTACG ATCCGGAAAC TGGTCAT

47

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single



31

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GTTCTCCTAT TAATGAAATA TCTTCATTAT GATGAAGAAA CTT

43

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

TACGCACTGG ATCCTTATAA GCAGCTTATT TTTACTGATT

40

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

GTTCTCCTCA TATGGAAACT CTGCCTCCAA AATACCTGCA

40

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear



32

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

TACGCACTGG ATCCTTATGT TGCATTTTCCT TTCTGAATTA GCA

43

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

CCGGAAACAG ATAATGAG

18

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GATCCTCATT ATCTGTTT

18

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA



33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

CCGGAAACAG AGAAGCCACG CAAAAGTAAG

30

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GATCCTTACT TTTGCGTGGC TTCTCTGTTT

30

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

TATGTTAATG AG

12

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA



34

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GATCCTCATT AACA

14

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

TATGTTCCGG AAACAGTTAA G

21

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GATCCTTAAC TGTTTCCGGA ACA

23

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:



35

TATGTTCCGG AAACAGTGAA TCAACTCAAA AATAAG

36

## (2) INFORMATION FOR SEQ ID NO:90:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GATCCTTATT TTTGAGTTGA TTCACTGTTT CCGGAACA

38

## (2) INFORMATION FOR SEQ ID NO:91:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

CTAGCGACGA CGACGACAAA GAACTCTGC CTCCAAAATA CCTGCATTAC GATCCGGAAA  
60

CTGGTCATCA GCTGCTGTGT GATAAATGTG CTCCGGGTAC

100

## (2) INFORMATION FOR SEQ ID NO:92:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:



36

CCGGAGCACA TTTATCACAC AGCAGCTGAT GACCAGTTTC CGGATCGTAA TGCAGGTATT  
60

TTGGAGGCAG AGTTTCTTTG TCGTCGTCGT CG

92

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ACAAACACAA TCGATTGAT ACTAGA

26

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

TTTGTTTAA CTAATTAAAG GAGGAATAAA ATATGAGAGG ATCGCATCAC

50

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

CATCACCATC ACGAAACCTT CCCGCCGAAA TACCTGCACT ACGACGAAGA 50

## (2) INFORMATION FOR SEQ ID NO:96:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

AACCTCCCAC CAGCTGCTGT GCGACAAATG CCCGCCGGGT ACCCAAACA 49

## (2) INFORMATION FOR SEQ ID NO:97:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

TGTTTGGGTA CCCGGCGGGC ATTTGT 26

## (2) INFORMATION FOR SEQ ID NO:98:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA



38

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

CGCAGCAGCAG CTGGTGGGAG GTTCTTCGT CGTAGTGCAG GTATTTCCGGC

50

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 49 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GGGAAGGTTT CGTGATGGTG ATGGTGATGC GATCCTCTCA TATTTTATT

49

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

CCTCCTTTAA TTAGTTAAAA CAAATCTAGT ATCAAATCGA TTGTGTTTGT

50

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:



39

ACAAACACAA TCGATTGAT ACTAGATTG TTTTAACTAA TTAAAGGAGG AATAAAATG  
59

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

CTAATTAAAG GAGGAATAAA ATGAAAGAAA CTTTTCCTCC AAAATATC

48

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

TGTTTGGGTA CCCGGCGGAC ATTTATCACA C

31

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:



40

ACAAACACAA TCGATTGAT ACTAGATTG TTCTAACTAA TTAAAGGAGG AATAAAATG  
59

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

CTAATTAAAG GAGGAATAAA ATGAAAAAAA AAGAACTTT TCCTCAAAA TATC  
54

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

TGTTTGGGTA CCCGGCGGAC ATTTATCACA C

31

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:



41

CAGCCCGGGT AAAATGGAAA CGTTTCCTCC AAAATATCTT CATT

44

## (2) INFORMATION FOR SEQ ID NO:108:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

CGTTTCATT TTACCCGGGC TGAGCGAGAG GCTCTTCTGC GTGT

44

## (2) INFORMATION FOR SEQ ID NO:109:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

CGCTCAGCCC GGGTAAAATG GAAACGTTGC CTCCAAAATA CCTGC

45

## (2) INFORMATION FOR SEQ ID NO:110:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

CCATTTTACC CGGGCTGAGC GAGAGGCTCT TCTGCGTGT

39



42

## (2) INFORMATION FOR SEQ ID NO:111:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GAAAATAAGC TGCTTAGCTG CAGCTGAACC AAAATC

36

## (2) INFORMATION FOR SEQ ID NO:112:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

CAGCTGCAGC TAAGCAGCTT ATTTTCACGG ATTG

34

## (2) INFORMATION FOR SEQ ID NO:113:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

AAAAATAAGC TGCTTAGCTG CAGCTGAACC AAAATC

36

## (2) INFORMATION FOR SEQ ID NO:114:



43

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

CAGCTGCAGC TAAGCAGCTT ATTTTACTG ATTGG

35

## (2) INFORMATION FOR SEQ ID NO:115:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

CTAGAAGGAG GAATAACATA TGGAACTTT TGCTCCAAAA TATCTTCATT ATGATGAAGA  
60

AACTAGTCAT CAGCTGCTGT GTGATAAATG TCCGCCGGGT AC

102

## (2) INFORMATION FOR SEQ ID NO:116:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:



44

CCGGCGGACA TTTATCACAC AGCAGCTGAT GACTAGTTTC TTCATCATAA TGAAGATATT  
60

TTGGAGCAAA AGTTTCATA TGTTATTCCT CCTT

94

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

CTAGAAGGAG GAATAACATA TGGAAACTTT TCCTGCTAAA TATCTTCATT ATGATGAAGA  
60

AA

62

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

CTAGTTTCTT CATCATAATG AAGATATTTA GCAGGAAAAG TTCCATATG TTATTCCTCC  
60

TT

62

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear



45

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Tyr His Tyr Tyr Asp Gln Asn Gly Arg Met Cys Glu Glu Cys His Met  
1 5 10 15

Cys Gln Pro Gly His Phe Leu Val Lys His Cys Lys Gln Pro Lys Arg  
20 25 30

Asp Thr Val Cys His Lys Pro Cys Glu Pro Gly Val Thr Tyr Thr Asp  
35 40 45

Asp Trp His  
50

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 124..1326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

ATCAAAGGCA GGGCATACTT CCTGTTGCCC AGACCTTATA TAAAACGTCA TGTTGCGCTG  
60

GGCAGCAGAG AAGCACCTAG CACTGGCCCA GCGGCTGCCG CCTGAGGTTT CCAGAGGACC  
120

ACA ATG AAC AAG TGG CTG TGC TGT GCA CTC CTG GTG TTC TTG GAC ATC  
168

Met Asn Lys Trp Leu Cys Cys Ala Leu Leu Val Phe Leu Asp Ile  
1 5 10 15



46

ATT GAA TGG ACA ACC CAG GAA ACC TTT CCT CCA AAA TAC TTG CAT TAT  
216

Ile Glu Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr  
20 25 30

GAC CCA GAA ACC GGA CGT CAG CTC TTG TGT GAC AAA TGT GCT CCT GGC  
264

Asp Pro Glu Thr Gly Arg Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly  
35 40 45

ACC TAC CTA AAA CAG CAC TGC ACA GTC AGG AGG AAG ACA CTG TGT GTC  
312

Thr Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys Thr Leu Cys Val  
50 55 60

CCT TGC CCT GAC TAC TCT TAT ACA GAC AGC TGG CAC ACG AGT GAT GAA  
360

Pro Cys Pro Asp Tyr Ser Tyr Thr Asp Ser Trp His Thr Ser Asp Glu  
65 70 75

TGC GTG TAC TGC AGC CCC GTG TGC AAG GAA CTG CAG ACC GTG AAA CAG  
408

Cys Val Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Thr Val Lys Gln  
80 85 90 95

GAG TGC AAC CGC ACC CAC AAC CGA GTG TGC GAA TGT GAG GAA GGG CGC  
456

Glu Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Glu Glu Gly Arg  
100 105 110

TAC CTG GAG CTC GAA TTC TGC TTG AAG CAC CGG AGC TGT CCC CCA GGC  
504

Tyr Leu Glu Leu Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly  
115 120 125

TTG GGT GTG CTG CAG GCT GGG ACC CCA GAG CGA AAC ACG GTT TGC AAA  
552

Leu Gly Val Leu Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys  
130 135 140

AGA TGT CCG GAT GGG TTC TTC TCA GGT GAG ACG TCA TCG AAA GCA CCC  
600

Arg Cys Pro Asp Gly Phe Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro  
145 150 155

TGT AGG AAA CAC ACC AAC TGC AGC TCA CTT GGC CTC CTG CTA ATT CAG  
648

Cys Arg Lys His Thr Asn Cys Ser Ser Leu Gly Leu Leu Leu Ile Gln  
160 165 170 175



47

AAA GGA AAT GCA ACA CAT GAC AAT GTA TGT TCC GGA AAC AGA GAA GCA  
696  
Lys Gly Asn Ala Thr His Asp Asn Val Cys Ser Gly Asn Arg Glu Ala  
180 185 190

ACT CAA AAT TGT GGA ATA GAT GTC ACC CTG TGC GAA GAG GCA TTC TTC  
744  
Thr Gln Asn Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe  
195 200 205

AGG TTT GCT GTG CCT ACC AAG ATT ATA CCG AAT TGG CTG AGT GTT CTG  
792  
Arg Phe Ala Val Pro Thr Lys Ile Ile Pro Asn Trp Leu Ser Val Leu  
210 215 220

GTG GAC AGT TTG CCT GGG ACC AAA GTG AAT GCA GAG AGT GTA GAG AGG  
840  
Val Asp Ser Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg  
225 230 235

ATA AAA CGG AGA CAC AGC TCG CAA GAG CAA ACT TTC CAG CTA CTT AAG  
888  
Ile Lys Arg Arg His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys  
240 245 250 255

CTG TGG AAG CAT CAA AAC AGA GAC CAG GAA ATG GTG AAG AAG ATC ATC  
936  
Leu Trp Lys His Gln Asn Arg Asp Gln Glu Met Val Lys Lys Ile Ile  
260 265 270

CAA GAC ATT GAC CTC TGT GAA AGC AGT GTG CAA CGG CAT ATC GGC CAC  
984  
Gln Asp Ile Asp Leu Cys Glu Ser Ser Val Gln Arg His Ile Gly His  
275 280 285

GCG AAC CTC ACC ACA GAG CAG CTC CGC ATC TTG ATG GAG AGC TTG CCT  
1032  
Ala Asn Leu Thr Thr Glu Gln Leu Arg Ile Leu Met Glu Ser Leu Pro  
290 295 300

GGG AAG AAG ATC AGC CCA GAC GAG ATT GAG AGA ACG AGA AAG ACC TGC  
1080  
Gly Lys Lys Ile Ser Pro Asp Glu Ile Glu Arg Thr Arg Lys Thr Cys  
305 310 315

AAA CCC AGC GAG CAG CTC CTG AAG CTA CTG AGC TTG TGG AGG ATC AAA  
1128  
Lys Pro Ser Glu Gln Leu Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys  
320 325 330 335

AAT GGA GAC CAA GAC ACC TTG AAG GGC CTG ATG TAC GCA CTC AAG CAC  
1176  
Asn Gly Asp Gln Asp Thr Leu Lys Gly Leu Met Tyr Ala Leu Lys His



48

340 345 350

TTG AAA GCA TAC CAC TTT CCC AAA ACC GTC ACC CAC AGT CTG AGG AAG  
1224Leu Lys Ala Tyr His Phe Pro Lys Thr Val Thr His Ser Leu Arg Lys  
355 360 365ACC ATC AGG TTC TTG CAC AGC TTC ACC ATG TAC CGA TTG TAT CAG AAA  
1272Thr Ile Arg Phe Leu His Ser Phe Thr Met Tyr Arg Leu Tyr Gln Lys  
370 375 380CTC TTT CTA GAA ATG ATA GGG AAT CAG GTT CAA TCA GTG AAG ATA AGC  
1320Leu Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser  
385 390 395TGC TTA TAGTTAGGAA TGGTCACTGG GCTGTTTCTT CAGGATGGGC CAACACTGAT  
1376Cys Leu  
400GGAGCAGATG GCTGCTTCTC CGGCTCTTGA AATGGCAGTT GATTCCTTTC TCATCAGTTG  
1436GTGGGAATGA AGATCCTCCA GCCCAACACA CAACTGGGG AGTCTGAGTC AGGAGAGTGA  
1496GGCAGGCTAT TTGATAATTG TGCAAAGCTG CCAGGTGTAC ACCTAGAAAG TCAAGCACCC  
1556TGAGAAAGAG GATATTTTTA TAACCTCAAA CATAGGCCCT TTCCTTCTC TCCTTATGGA  
1616TGAGTACTCA GAAGGCTTCT ACTATCTTCT GTGTCATCCC TAGATGAAGG CCTCTTTTAT  
1676TTATTTTTTT ATTCTTTTTT TCGGAGCTGG GGACCGAACC CAGGGCCTTG CGCTTGCGAG  
1736GCAAGTGCTC TACCACTGAG CTAAATCTCC AACCCCTGAA GGCCTCTTTC TTTCTGCCTC  
1796TGATAGTCTA TGACATTCTT TTTTCTACAA TTCGTATCAG GTGCACGAGC CTTATCCCAT  
1856TTGTAGGTTT CTAGGCAAGT TGACCGTTAG CTATTTTTCC CTCTGAAGAT TTGATTCGAG  
1916TTGCAGACTT GGCTAGACAA GCAGGGGTAG GTTATGGTAG TTTATTTAAC AGACTGCCAC  
1976



49

CAGGAGTCCA GTGTTTCTTG TTCCTCTGTA GTGTACCTA AGCTGACTCC AAGTACATTT  
2036

AGTATGAAAA ATAATCAACA AATTTTATTC CTTCTATCAA CATTGGCTAG CTTTGTTC  
2096

GGGCACTAAA AGAACTACT ATATGGAGAA AGAATTGATA TGGCCCCCAA CGTCAACAA  
2156

CCCAATAGTT TATCCAGCTG TCATGCCTGG TTCAGTGTCT ACTGACTATG CGCCCTCTTA  
2216

TTACTGCATG CAGTAATTCA ACTGGAAATA GTAATAATAA TAATAGAAAT AAAATCTAGA  
2276

CTCCATTGGA TCTCTCTGAA TATGGGAATA TCTAACTTAA GAAGCTTTGA GATTCAGTT  
2336

GTGTTAAAGG CTTTATTAA AAAGCTGATG CTCTTCTGTA AAAGTTACTA ATATATCTGT  
2396

AAGACTATTA CAGTATTGCT ATTTATATCC ATCCAG

2432

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 401 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Met Asn Lys Trp Leu Cys Cys Ala Leu Leu Val Phe Leu Asp Ile Ile  
1 5 10 15

Glu Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
20 25 30

Pro Glu Thr Gly Arg Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly Thr  
35 40 45

Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys Thr Leu Cys Val Pro  
50 55 60

Cys Pro Asp Tyr Ser Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys  
65 70 75 80



50

Val Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Thr Val Lys Gln Glu  
85 90 95

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Glu Glu Gly Arg Tyr  
100 105 110

Leu Glu Leu Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Leu  
115 120 125

Gly Val Leu Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg  
130 135 140

Cys Pro Asp Gly Phe Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro Cys  
145 150 155 160

Arg Lys His Thr Asn Cys Ser Ser Leu Gly Leu Leu Leu Ile Gln Lys  
165 170 175

Gly Asn Ala Thr His Asp Asn Val Cys Ser Gly Asn Arg Glu Ala Thr  
180 185 190

Gln Asn Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg  
195 200 205

Phe Ala Val Pro Thr Lys Ile Ile Pro Asn Trp Leu Ser Val Leu Val  
210 215 220

Asp Ser Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile  
225 230 235 240

Lys Arg Arg His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu  
245 250 255

Trp Lys His Gln Asn Arg Asp Gln Glu Met Val Lys Lys Ile Ile Gln  
260 265 270

Asp Ile Asp Leu Cys Glu Ser Ser Val Gln Arg His Ile Gly His Ala  
275 280 285

Asn Leu Thr Thr Glu Gln Leu Arg Ile Leu Met Glu Ser Leu Pro Gly  
290 295 300



51

ys Lys Ile Ser Pro Asp Glu Ile Glu Arg Thr Arg Lys Thr Cys Lys  
 305            310            315            320

Pro Ser Glu Gln Leu Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn  
       325            330            335

Gly Asp Gln Asp Thr Leu Lys Gly Leu Met Tyr Ala Leu Lys His Leu  
       340            345            350

Lys Ala Tyr His Phe Pro Lys Thr Val Thr His Ser Leu Arg Lys Thr  
       355            360            365

Ile Arg Phe Leu His Ser Phe Thr Met Tyr Arg Leu Tyr Gln Lys Leu  
       370            375            380

Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys  
       385            390            395            400

Leu

## (2) INFORMATION FOR SEQ ID NO:122:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 90..1292

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

CCTTATATAA ACGTCATGAT TGCCTGGGCT GCAGAGACGC ACCTAGCACT GACCCAGCGG  
 60

CTGCCTCCTG AGGTTTCCCG AGGACCACA ATG AAC AAG TGG CTG TGC TGC GCA  
 113

Met Asn Lys Trp Leu Cys Cys Ala  
       1            5

CTC CTG GTG CTC CTG GAC ATC ATT GAA TGG ACA ACC CAG GAA ACC CTT  
 161

Leu Leu Val Leu Leu Asp Ile Ile Glu Trp Thr Thr Gln Glu Thr Leu  
       10            15            20



52

CCT CCA AAG TAC TTG CAT TAT GAC CCA GAA ACT GGT CAT CAG CTC CTG  
209

Pro Pro Lys Tyr Leu His Tyr Asp Pro Glu Thr Gly His Gln Leu Leu  
25 30 35 40

TGT GAC AAA TGT GCT CCT GGC ACC TAC CTA AAA CAG CAC TGC ACA GTG  
257

Cys Asp Lys Cys Ala Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Val  
45 50 55

AGG AGG AAG ACA TTG TGT GTC CCT TGC CCT GAC CAC TCT TAT ACG GAC  
305

Arg Arg Lys Thr Leu Cys Val Pro Cys Pro Asp His Ser Tyr Thr Asp  
60 65 70

AGC TGG CAC ACC AGT GAT GAG TGT GTG TAT TGC AGC CCA GTG TGC AAG  
353

Ser Trp His Thr Ser Asp Glu Cys Val Tyr Cys Ser Pro Val Cys Lys  
75 80 85

GAA CTG CAG TCC GTG AAG CAG GAG TGC AAC CGC ACC CAC AAC CGA GTG  
401

Glu Leu Gln Ser Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val  
90 95 100

TGT GAG TGT GAG GAA GGG CGT TAC CTG GAG ATC GAA TTC TGC TTG AAG  
449

Cys Glu Cys Glu Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys  
105 110 115 120

CAC CGG AGC TGT CCC CCG GGC TCC GGC GTG GTG CAA GCT GGA ACC CCA  
497

His Arg Ser Cys Pro Pro Gly Ser Gly Val Val Gln Ala Gly Thr Pro  
125 130 135

GAG CGA AAC ACA GTT TGC AAA AAA TGT CCA GAT GGG TTC TTC TCA GGT  
545

Glu Arg Asn Thr Val Cys Lys Lys Cys Pro Asp Gly Phe Phe Ser Gly  
140 145 150

GAG ACT TCA TCG AAA GCA CCC TGT ATA AAA CAC ACG AAC TGC AGC ACA  
593

Glu Thr Ser Ser Lys Ala Pro Cys Ile Lys His Thr Asn Cys Ser Thr  
155 160 165

TTT GGC CTC CTG CTA ATT CAG AAA GGA AAT GCA ACA CAT GAC AAC GTG  
641

Phe Gly Leu Leu Leu Ile Gln Lys Gly Asn Ala Thr His Asp Asn Val  
170 175 180

TGT TCC GGA AAC AGA GAA GCC ACG CAA AAG TGT GGA ATA GAT GTC ACC  
689

Cys Ser Gly Asn Arg Glu Ala Thr Gln Lys Cys Gly Ile Asp Val Thr



53

185                      190                      195                      200  
 CTG TGT GAA GAG GCC TTC TTC AGG TTT GCT GTT CCT ACC AAG ATT ATA  
 737  
 Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr Lys Ile Ile  
           205                      210                      215  
  
 CCA AAT TGG CTG AGT GTT TTG GTG GAC AGT TTG CCT GGG ACC AAA GTG  
 785  
 Pro Asn Trp Leu Ser Val Leu Val Asp Ser Leu Pro Gly Thr Lys Val  
           220                      225                      230  
  
 AAT GCC GAG AGT GTA GAG AGG ATA AAA CGG AGA CAC AGC TCA CAA GAG  
 833  
 Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Arg His Ser Ser Gln Glu  
           235                      240                      245  
  
 CAA ACC TTC CAG CTG CTG AAG CTG TGG AAA CAT CAA AAC AGA GAC CAG  
 881  
 Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn Arg Asp Gln  
           250                      255                      260  
  
 GAA ATG GTG AAG AAG ATC ATC CAA GAC ATT GAC CTC TGT GAA AGC AGC  
 929  
 Glu Met Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys Glu Ser Ser  
 265                      270                      275                      280  
  
 GTG CAG CGG CAT CTC GGC CAC TCG AAC CTC ACC ACA GAG CAG CTT CTT  
 977  
 Val Gln Arg His Leu Gly His Ser Asn Leu Thr Thr Glu Gln Leu Leu  
           285                      290                      295  
  
 GCC TTG ATG GAG AGC CTG CCT GGG AAG AAG ATC AGC CCA GAA GAG ATT  
 1025  
 Ala Leu Met Glu Ser Leu Pro Gly Lys Lys Ile Ser Pro Glu Glu Ile  
           300                      305                      310  
  
 GAG AGA ACG AGA AAG ACC TGC AAA TCG AGC GAG CAG CTC CTG AAG CTA  
 1073  
 Glu Arg Thr Arg Lys Thr Cys Lys Ser Ser Glu Gln Leu Leu Lys Leu  
           315                      320                      325  
  
 CTC AGT TTA TGG AGG ATC AAA AAT GGT GAC CAA GAC ACC TTG AAG GGC  
 1121  
 Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys Gly  
           330                      335                      340  
  
 CTG ATG TAT GCC CTC AAG CAC TTG AAA ACA TCC CAC TTT CCC AAA ACT  
 1169  
 Leu Met Tyr Ala Leu Lys His Leu Lys Thr Ser His Phe Pro Lys Thr  
 345                      350                      355                      360



54

GTC ACC CAC AGT CTG AGG AAG ACC ATG AGG TTC CTG CAC AGC TTC ACA  
1217  
Val Thr His Ser Leu Arg Lys Thr Met Arg Phe Leu His Ser Phe Thr  
365 370 375

ATG TAC AGA CTG TAT CAG AAG CTC TTT TTA GAA ATG ATA GGG AAT CAG  
1265  
Met Tyr Arg Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly Asn Gln  
380 385 390

GTT CAA TCC GTG AAA ATA AGC TGC TTA TAACTAGGAA TGGTCACTGG  
1312  
Val Gln Ser Val Lys Ile Ser Cys Leu  
395 400

GCTGTTTCTT CA 1324

## (2) INFORMATION FOR SEQ ID NO:123:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Met Asn Lys Trp Leu Cys Cys Ala Leu Leu Val Leu Leu Asp Ile Ile  
1 5 10 15  
Glu Trp Thr Thr Gln Glu Thr Leu Pro Pro Lys Tyr Leu His Tyr Asp  
20 25 30  
Pro Glu Thr Gly His Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly Thr  
35 40 45  
Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys Thr Leu Cys Val Pro  
50 55 60  
Cys Pro Asp His Ser Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys  
65 70 75 80  
Val Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Ser Val Lys Gln Glu  
85 90 95  
Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Glu Glu Gly Arg Tyr  
100 105 110  
Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Ser



115                      120                      125

Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys  
385                    390                    395                    400



Leu

## (2) INFORMATION FOR SEQ ID NO:124:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 94..1296

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GTATATATAA CGTGATGAGC GTACGGGTGC GGAGACGCAC CGGAGCGCTC GCCCAGCCGC  
60

CGCTCCAAGC CCCTGAGGTT TCCGGGGACC ACA ATG AAC AAG TTG CTG TGC TGC  
114

Met Asn Lys Leu Leu Cys Cys  
1 5

GCG CTC GTG TTT CTG GAC ATC TCC ATT AAG TGG ACC ACC CAG GAA ACG  
162

Ala Leu Val Phe Leu Asp Ile Ser Ile Lys Trp Thr Thr Gln Glu Thr  
10 15 20

TTT CCT CCA AAG TAC CTT CAT TAT GAC GAA GAA ACC TCT CAT CAG CTG  
210

Phe Pro Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser His Gln Leu  
25 30 35

TTG TGT GAC AAA TGT CCT CCT GGT ACC TAC CTA AAA CAA CAC TGT ACA  
258

Leu Cys Asp Lys Cys Pro Pro Gly Thr Tyr Leu Lys Gln His Cys Thr  
40 45 50 55

GCA AAG TGG AAG ACC GTG TGC GCC CCT TGC CCT GAC CAC TAC TAC ACA  
306

Ala Lys Trp Lys Thr Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr  
60 65 70

GAC AGC TGG CAC ACC AGT GAC GAG TGT CTA TAC TGC AGC CCC GTG TGC  
354

Asp Ser Trp His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys



57

75	80	85	
AAG GAG CTG CAG TAC GTC	AAG CAG GAG TGC AAT CGC ACC CAC AAC CGC		
402			
Lys Glu Leu Gln Tyr Val	Lys Gln Glu Cys Asn Arg Thr His Asn Arg		
90	95	100	
GTG TGC GAA TGC AAG GAA GGG CGC TAC CTT GAG ATA GAG TTC TGC TTG			
450			
Val Cys Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu			
105	110	115	
AAA CAT AGG AGC TGC CCT CCT GGA TTT GGA GTG GTG CAA GCT GGA ACC			
498			
Lys His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr			
120	125	130	135
CCA GAG CGA AAT ACA GTT TGC AAA AGA TGT CCA GAT GGG TTC TTC TCA			
546			
Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe Ser			
140	145	150	
AAT GAG ACG TCA TCT AAA GCA CCC TGT AGA AAA CAC ACA AAT TGC AGT			
594			
Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn Cys Ser			
155	160	165	
GTC TTT GGT CTC CTG CTA ACT CAG AAA GGA AAT GCA ACA CAC GAC AAC			
642			
Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr His Asp Asn			
170	175	180	
ATA TGT TCC GGA AAC AGT GAA TCA ACT CAA AAA TGT GGA ATA GAT GTT			
690			
Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile Asp Val			
185	190	195	
ACC CTG TGT GAG GAG GCA TTC TTC AGG TTT GCT GTT CCT ACA AAG TTT			
738			
Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr Lys Phe			
200	205	210	215
ACG CCT AAC TGG CTT AGT GTC TTG GTA GAC AAT TTG CCT GGC ACC AAA			
786			
Thr Pro Asn Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly Thr Lys			
220	225	230	
GTA AAC GCA GAG AGT GTA GAG AGG ATA AAA CGG CAA CAC AGC TCA CAA			
834			
Val Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser Ser Gln			
235	240	245	



58

GAA CAG ACT TTC CAG CTG CTG AAG TTA TGG AAA CAT CAA AAC AAA GCC  
882

Glu Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn Lys Ala  
250 255 260

CAA GAT ATA GTC AAG AAG ATC ATC CAA GAT ATT GAC CTC TGT GAA AAC  
930

Gln Asp Ile Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys Glu Asn  
265 270 275

AGC GTG CAG CGG CAC ATT GGA CAT GCT AAC CTC ACC TTC GAG CAG CTT  
978

Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr Phe Glu Gln Leu  
280 285 290 295

CGT AGC TTG ATG GAA AGC TTA CCG GGA AAG AAA GTG GGA GCA GAA GAC  
1026

Arg Ser Leu Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala Glu Asp  
300 305 310

ATT GAA AAA ACA ATA AAG GCA TGC AAA CCC AGT GAC CAG ATC CTG AAG  
1074

Ile Glu Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile Leu Lys  
315 320 325

CTG CTC AGT TTG TGG CGA ATA AAA AAT GGC GAC CAA GAC ACC TTG AAG  
1122

Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr Leu Lys  
330 335 340

GGC CTA ATG CAC GCA CTA AAG CAC TCA AAG ACG TAC CAC TTT CCC AAA  
1170

Gly Leu Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe Pro Lys  
345 350 355

ACT GTC ACT CAG AGT CTA AAG AAG ACC ATC AGG TTC CTT CAC AGC TTC  
1218

Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His Ser Phe  
360 365 370 375

ACA ATG TAC AAA TTG TAT CAG AAG TTA TTT TTA GAA ATG ATA GGT AAC  
1266

Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile Gly Asn  
380 385 390

CAG GTC CAA TCA GTA AAA ATA AGC TGC TTA TAACTGGAAA TGGCCATTGA  
1316

Gln Val Gln Ser Val Lys Ile Ser Cys Leu  
395 400

GCTGTTTCCT CACAATTGGC GAGATCCCAT GGATGATAA

1355



59

## (2) INFORMATION FOR SEQ ID NO:125:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

```

Met Asn Lys Leu Leu Cys Cys Ala Leu Val Phe Leu Asp Ile Ser Ile
 1         5         10        15

Lys Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp
 20        25        30

Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr
 35         40        45

Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro
 50         55        60

Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys
 65         70        75        80

Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu
 85         90        95

Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr
100        105       110

Leu Glu Ile Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe
115        120       125

Gly Val Val Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg
130        135       140

Cys Pro Asp Gly Phe Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys
145        150       155       160

Arg Lys His Thr Asn Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys
165        170       175

Gly Asn Ala Thr His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr
180        185       190

Gln Lys Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg
195        200       205

Phe Ala Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val
210        215       220

```



60

Asp Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile  
 225 230 235 240

Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu  
 245 250 255

Trp Lys His Gln Asn Lys Ala Gln Asp Ile Val Lys Lys Ile Ile Gln  
 260 265 270

Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile Gly His Ala  
 275 280 285

Asn Leu Thr Phe Glu Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly  
 290 295 300

Lys Lys Val Gly Ala Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys  
 305 310 315 320

Pro Ser Asp Gln Ile Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn  
 325 330 335

Gly Asp Gln Asp Thr Leu Lys Gly Leu Met His Ala Leu Lys His Ser  
 340 345 350

Lys Thr Tyr His Phe Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr  
 355 360 365

Ile Arg Phe Leu His Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu  
 370 375 380

Phe Leu Glu Met Ile Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys  
 385 390 395 400

Leu

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein .

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys  
 1 5 10 15



61

Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro  
 20 25 30  
 Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala  
 35 40 45  
 Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys  
 50 55 60  
 Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr  
 65 70 75 80  
 Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn  
 85 90 95  
 Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His  
 100 105 110  
 Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly  
 115 120 125  
 Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys  
 130 135

## (2) INFORMATION FOR SEQ ID NO:127:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

CCGGCGGACA TTTATCACAC AGCAGCTGAT GAGAAGTTTC TTCATCCA

48

## (2) INFORMATION FOR SEQ ID NO:128:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids



62

(B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

```

Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu Thr Ser Val Ala
1      5      10      15

Arg Leu Ser Ser Lys Ser Val Asn Ala Gln Val Thr Asp Ile Asn Ser
      20      25      30

Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val Glu Thr Gln Asn
      35      40      45

Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro
      50      55      60

Pro Gly Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro
      65      70      75      80

Asp Cys Val Pro Cys Gln Glu Gly Lys Glu Tyr Thr Asp Lys Ala His
      85      90      95

Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly His Gly
      100     105     110

Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg
      115     120     125

Cys Lys Pro Asn Phe Phe Cys Asn Ser Thr Val Cys Glu His Cys Asp
      130     135     140

Pro Cys Thr Lys Cys Glu His Gly Ile Ile Lys Glu Cys Thr Leu Thr
      145     150     155     160

Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser Asn Leu Gly Trp
      165     170     175

Leu Cys Leu Leu Leu Leu Pro Ile Pro Leu Ile Val Trp Val Lys Arg
      180     185     190

Lys Glu Val Gln Lys Thr Cys Arg Lys His Arg Lys Glu Asn Gln Gly
      195     200     205

Ser His Glu Ser Pro Thr Leu Asn Pro Glu Thr
      210     215

```



## (2) INFORMATION FOR SEQ ID NO:129:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

```

Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu
 1      5      10      15

Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
 20      25      30

His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
 35      40      45

Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
 50      55      60

Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
 65      70      75      80

Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
 85      90      95

Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
100      105      110

Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
115      120      125

Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
130      135      140

Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
145      150      155      160

Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
165      170      175

Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
180      185      190

Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
195      200      205

```



64

Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu  
 210                    215                    220  
 Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys  
 225                    230                    235                    240  
 Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu  
 245                    250                    255  
 Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser  
 260                    265                    270  
 Phe Ser Pro Thr Pro Gly Phe Thr  
 275                    280

## (2) INFORMATION FOR SEQ ID NO:130:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Met Leu Arg Leu Ile Ala Leu Leu Val Cys Val Val Tyr Val Tyr Gly  
 1                    5                    10                    15  
 Asp Asp Val Pro Tyr Ser Ser Asn Gln Gly Lys Cys Gly Gly His Asp  
 20                    25                    30  
 Tyr Glu Lys Asp Gly Leu Cys Cys Ala Ser Cys His Pro Gly Phe Tyr  
 35                    40                    45  
 Ala Ser Arg Leu Cys Gly Pro Gly Ser Asn Thr Val Cys Ser Pro Cys  
 50                    55                    60  
 Glu Asp Gly Thr Phe Thr Ala Ser Thr Asn His Ala Pro Ala Cys Val  
 65                    70                    75                    80  
 Ser Cys Arg Gly Pro Cys Thr Gly His Leu Ser Glu Ser Gln Pro Cys  
 85                    90                    95



65

Asp Arg Thr His Asp Arg Val Cys Asn Cys Ser Thr Gly Asn Tyr Cys  
 100 105 110

Leu Leu Lys Gly Gln Asn Gly Cys Arg Ile Cys Ala Pro Gln Thr Lys  
 115 120 125

Cys Pro Ala Gly Tyr Gly Val Ser Gly His Thr Arg Ala Gly Asp Thr  
 130 135 140

Leu Cys Glu Lys Cys Pro Pro His Thr Tyr Ser Asp Ser Leu Ser Pro  
 145 150 155 160

Thr Glu Arg Cys Gly Thr Ser Phe Asn Tyr Ile Ser Val Gly Phe Asn  
 165 170 175

Leu Tyr Pro Val Asn Glu Thr Ser Cys Thr Thr Thr Ala Gly His Asn  
 180 185 190

Glu Val Ile Lys Thr Lys Glu Phe Thr Val Thr Leu Asn Tyr Thr  
 195 200 205

## (2) INFORMATION FOR SEQ ID NO:131:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

~~Met~~ ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu  
 1 5 10 15

Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr  
 20 25 30

Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln  
 35 40 45

Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys  
 50 55 60

Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp  
 65 70 75 80

Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys  
 85 90 95



66

Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg  
 100 105 110  
 Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu  
 115 120 125  
 Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg  
 130 135 140  
 Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val  
 145 150 155 160  
 Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr  
 165 170 175  
 Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly  
 180 185 190  
 Asn Ala Ser Arg Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser  
 195 200 205  
 Met ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser  
 210 215 220  
 Gln His Thr  
 225

## (2) INFORMATION FOR SEQ ID NO:132:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Met Val Ser Leu Pro Arg Leu Cys Ala Leu Trp Gly Cys Leu Leu Thr  
 1 5 10 15  
 Ala Val His Leu Gly Gln Cys Val Thr Cys Ser Asp Lys Gln Tyr Leu  
 20 25 30  
 His Asp Gly Gln Cys Cys Asp Leu Cys Gln Pro Gly Ser Arg Leu Thr  
 35 40 45



67

Ser His Cys Thr Ala Leu Glu Lys Thr Gln Cys His Pro Cys Asp Ser  
50 55 60

Gly Glu Phe Ser Ala Gln Trp Asn Arg Glu Ile Arg Cys His Gln His  
65 70 75 80

Arg His Cys Glu Pro Asn Gln Gly Leu Arg Val Lys Lys Glu Gly Thr  
85 90 95

Ala Glu Ser Asp Thr Val Cys Thr Cys Lys Glu Gly Gln His Cys Thr  
100 105 110

Ser Lys Asp Cys Glu Ala Cys Ala Gln His Thr Pro Cys Ile Pro Gly  
115 120 125

Phe Gly Val Met Glu Met ala Thr Glu Thr Thr Asp Thr Val Cys His  
130 135 140

Pro Cys Pro Val Gly Phe Phe Ser Asn Gln Ser Ser Leu Phe Glu Lys  
145 150 155 160

Cys Tyr Pro Trp Thr Ser Cys Glu Asp Lys Asn Leu Glu Val Leu Gln  
165 170 175

Lys Gly Thr Ser Gln Thr Asn Val Ile Cys Gly Leu Lys Ser Arg Met  
180 185 190

Arg Ala Leu Leu Val  
195

## (2) INFORMATION FOR SEQ ID NO:133:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Met Asn Lys Trp Leu Cys Cys Ala Leu Leu Val Phe Leu Asp Ile Ile  
1 5 10 15

Glu Trp Thr Thr Gln Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp  
20 25 30

Pro Glu Thr Gly Arg Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly Thr  
35 40 45



68

Tyr Leu Lys Gln His Cys Thr Val Arg Arg Lys Thr Leu Cys Val Pro  
 50                      55                      60  
 Cys Pro Asp Tyr Ser Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys  
 65                      70                      75                      80  
 Val Tyr Cys Ser Pro Val Cys Lys Glu Leu Gln Thr Val Lys Gln Glu  
 85                      90                      95  
 Cys Asn Arg Thr His Asn Arg Val Cys Glu Cys Glu Glu Gly Arg Tyr  
 100                      105                      110  
 Leu Glu Leu Glu Phe Cys Leu Lys His Arg Ser Cys Pro Pro Gly Leu  
 115                      120                      125  
 Gly Val Leu Gln Ala Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg  
 130                      135                      140  
 Cys Pro Asp Gly Phe Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro Cys  
 145                      150                      155                      160  
 Arg Lys His Thr Asn Cys Ser Ser Leu Gly Leu Leu Leu Ile Gln Lys  
 165                      170                      175  
 Gly Asn Ala Thr His Asp Asn Val Cys Ser Gly Asn Arg Glu Ala Thr  
 180                      185                      190  
 Gln Asn Cys Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg  
 195                      200                      205

## (2) INFORMATION FOR SEQ ID NO:134:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Met Gly Ala Gly Ala Thr Gly Arg Ala Met Asp Gly Pro Arg Leu Leu  
 1                      5                      10                      15  
 Leu Leu Leu Leu Leu Gly Val Ser Leu Gly Gly Ala Lys Glu Ala Cys  
 20                      25                      30  
 Pro Thr Gly Leu Tyr Thr His Ser Gly Glu Cys Cys Lys Ala Cys Asn  
 35                      40                      45



69

Leu Gly Glu Gly Val Ala Gln Pro Cys Gly Ala Asn Gln Thr Val Cys  
 50                    55                    60

Glu Pro Cys Leu Asp Ser Val Thr Phe Ser Asp Val Val Ser Ala Thr  
 65                    70                    75                    80

Glu Pro Cys Lys Pro Cys Thr Glu Cys Val Gly Leu Gln Ser Met Ser  
 85                    90                    95

Ala Pro Cys Val Glu Ala Asp Asp Ala Val Cys Arg Cys Ala Tyr Gly  
 100                    105                    110

Tyr Tyr Gln Asp Glu Thr Thr Gly Arg Cys Glu Ala Cys Arg Val Cys  
 115                    120                    125

Glu Ala Gly Ser Gly Leu Val Phe Ser Cys Gln Asp Lys Gln Asn Thr  
 130                    135                    140

Val Cys Glu Glu Cys Pro Asp Gly Thr Tyr Ser Asp Glu Ala Asn His  
 145                    150                    155                    160

Val Asp Pro Cys Leu Pro Cys Thr Val Cys Glu Asp Thr Glu Arg Gln  
 165                    170                    175

Leu Arg Glu Cys Thr Arg Trp Ala Asp Ala Glu Cys Glu Glu Ile Pro  
 180                    185                    190

Gly Arg Trp Ile Thr Arg Ser Thr Pro Pro Glu Gly Ser Asp Ser Thr  
 195                    200                    205

Ala Pro Ser Thr Gln Glu Pro Glu Ala Pro Pro Glu Gln Asp Leu Ile  
 210                    215                    220

## (2) INFORMATION FOR SEQ ID NO:135:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Met Tyr Val Trp Val Gln Gln Pro Thr Ala Phe Leu Leu Leu Gly Leu  
 1                    5                    10                    15

Ser Leu Gly Val Thr Val Lys Leu Asn Cys Val Lys Asp Thr Tyr Pro  
 20                    25                    30



70

Ser Gly His Lys Cys Cys Arg Glu Cys Gln Pro Gly His Gly Met Val  
 35 40 45  
 Ser Arg Cys Asp His Thr Arg Asp Thr Val Cys His Pro Cys Glu Pro  
 50 55 60  
 Gly Phe Tyr Asn Glu Ala Val Asn Tyr Asp Thr Cys Lys Gln Cys Thr  
 65 70 75 80  
 Gln Cys Asn His Arg Ser Gly Ser Glu Leu Lys Gln Asn Cys Thr Pro  
 85 90 95  
 Thr Glu Asp Thr Val Cys Gln Cys Arg Pro Gly Thr Gln Pro Arg Gln  
 100 105 110  
 Asp Ser Ser His Lys Leu Gly Val Asp Cys Val Pro Cys Pro Pro Gly  
 115 120 125  
 His Phe Ser Pro Gly Ser Asn Gln Ala Cys Lys Pro Trp Thr Asn Cys  
 130 135 140  
 Thr Leu Ser Gly Lys Gln Ile Arg His Pro Ala Ser Asn Ser Leu Asp  
 145 150 155 160  
 Thr Val Cys Glu Asp Arg Ser Leu Leu Ala Thr Leu Leu Trp Glu Thr  
 165 170 175  
 Gln Arg Thr Thr Phe Arg Pro Thr Thr Val Pro Ser Thr Thr Val Trp  
 180 185 190  
 Pro Arg Thr Ser Gln Leu Pro Ser Thr Pro Thr Leu Val  
 195 200 205

## (2) INFORMATION FOR SEQ ID NO:136:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Met Gly Asn Asn Cys Tyr Asn Val Val Val Ile Val Leu Leu Leu Val  
 1 5 10 15



71

Gly Cys Glu Lys Val Gly Ala Val Gln Asn Ser Cys Asp Asn Cys Gln  
 20 25 30

Pro Gly Thr Phe Cys Arg Lys Tyr Asn Pro Val Cys Lys Ser Cys Pro  
 35 40 45

Pro Ser Thr Phe Ser Ser Ile Gly Gly Gln Pro Asn Cys Asn Ile Cys  
 50 55 60

Arg Val Cys Ala Gly Tyr Phe Arg Phe Lys Lys Phe Cys Ser Ser Thr  
 65 70 75 80

His Asn Ala Glu Cys Glu Cys Ile Glu Gly Phe His Cys Leu Gly Pro  
 85 90 95

Gln Cys Thr Arg Cys Glu Lys Asp Cys Arg Pro Gly Gln Glu Leu Thr  
 100 105 110

Lys Gln Gly Cys Lys Thr Cys Ser Leu Gly Thr Phe Asn Asp Gln Asn  
 115 120 125

Gly Thr Gly Val Cys Arg Pro Trp Thr Asn Cys Ser Leu Asp Gly Arg  
 130 135 140

Ser Val Leu Lys Thr Gly Thr Thr Glu Lys Asp Val Val Cys Gly Pro  
 145 150 155 160

Pro Val Val Ser Phe Ser Pro Ser Thr Thr Ile Ser Val Thr Pro Glu  
 165 170 175

Gly Gly Pro Gly Gly His Ser Leu Gln Val Leu Thr Leu Phe Leu  
 180 185 190

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

TATGGATGAA GAAACTTCTC ATCAGCTGCT GTGTGATAAA TGTCCGCCGG GTAC  
 54

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 amino acids



72

(B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

```

Glu Thr Leu Pro Pro Lys Tyr Leu His Tyr Asp Pro Glu Thr Gly His
1      5      10      15

Gln Leu Leu Cys Asp Lys Cys Ala Pro Gly Thr Tyr Leu Lys Gln His
20     25     30

Cys Thr Val Arg Arg Lys Thr Leu Cys Val Pro Cys Pro Asp His Ser
35     40     45

Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys Val Tyr Cys Ser Pro
50     55     60

Val Cys Lys Glu Leu Gln Ser Val Lys Gln Glu Cys Asn Arg Thr His
65     70     75     80

Asn Arg Val Cys Glu Cys Glu Glu Gly Arg Tyr Leu Glu Ile Glu Phe
85     90     95

Cys Leu Lys His Arg Ser Cys Pro Pro Gly Ser Gly Val Val Gln Ala
100    105    110

Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Lys Cys Pro Asp Gly Phe
115    120    125

Phe Ser Gly Glu Thr Ser Ser Lys Ala Pro Cys Ile Lys His Thr Asn
130    135    140

Cys Ser Thr Phe Gly Leu Leu Leu Ile Gln Lys Gly Asn Ala Thr His
145    150    155    160

Asp Asn Val Cys Ser Gly Asn Arg Glu Ala Thr Gln Lys Cys Gly Ile
165    170    175

Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr
180    185    190

Lys Ile Ile Pro Asn Trp Leu Ser Val Leu Val Asp Ser Leu Pro Gly
195    200    205

Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Arg His Ser
210    215    220

Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn

```



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225	230	235	240
Arg Asp Gln Glu Met Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys			
245	250	255	
Glu Ser Ser Val Gln Arg His Leu Gly His Ser Asn Leu Thr Thr Glu			
260	265	270	
Gln Leu Leu Ala Leu Met Glu Ser Leu Pro Gly Lys Lys Ile Ser Pro			
275	280	285	
Glu Glu Ile Glu Arg Thr Arg Lys Thr Cys Lys Ser Ser Glu Gln Leu			
290	295	300	
Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr			
305	310	315	320
Leu Lys Gly Leu Met Tyr Ala Leu Lys His Leu Lys Thr Ser His Phe			
325	330	335	
Pro Lys Thr Val Thr His Ser Leu Arg Lys Thr Met Arg Phe Leu His			
340	345	350	
Ser Phe Thr Met Tyr Arg Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile			
355	360	365	
Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu			
370	375	380	

## (2) INFORMATION FOR SEQ ID NO:139:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

Glu Thr Phe Pro Pro Lys Tyr Leu His Tyr Asp Glu Glu Thr Ser His
1            5            10            15
Gln Leu Leu Cys Asp Lys Cys Pro Pro Gly Thr Tyr Leu Lys Gln His
20            25            30
Cys Thr Ala Lys Trp Lys Thr Val Cys Ala Pro Cys Pro Asp His Tyr
35            40            45



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Tyr Thr Asp Ser Trp His Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro  
 50 55 60

Val Cys Lys Glu Leu Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His  
 65 70 75 80

Asn Arg Val Cys Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe  
 85 90 95

Cys Leu Lys His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala  
 100 105 110

Gly Thr Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe  
 115 120 125

Phe Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn  
 130 135 / 140

Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr His  
 145 150 155 160

Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys Gly Ile  
 165 170 175

Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala Val Pro Thr  
 180 185 190

Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp Asn Leu Pro Gly  
 195 200 205

Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile Lys Arg Gln His Ser  
 210 215 220

Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys Leu Trp Lys His Gln Asn  
 225 230 235 240

Lys Ala Gln Asp Ile Val Lys Lys Ile Ile Gln Asp Ile Asp Leu Cys  
 245 250 255

Glu Asn Ser Val Gln Arg His Ile Gly His Ala Asn Leu Thr Phe Glu  
 260 265 270

Gln Leu Arg Ser Leu Met Glu Ser Leu Pro Gly Lys Lys Val Gly Ala  
 275 280 285

Glu Asp Ile Glu Lys Thr Ile Lys Ala Cys Lys Pro Ser Asp Gln Ile  
 290 295 300

Leu Lys Leu Leu Ser Leu Trp Arg Ile Lys Asn Gly Asp Gln Asp Thr  
 305 310 315 320

Leu Lys Gly Leu Met His Ala Leu Lys His Ser Lys Thr Tyr His Phe



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325 330 335  
Pro Lys Thr Val Thr Gln Ser Leu Lys Lys Thr Ile Arg Phe Leu His  
340 345 350  
Ser Phe Thr Met Tyr Lys Leu Tyr Gln Lys Leu Phe Leu Glu Met Ile  
355 360 365  
Gly Asn Gln Val Gln Ser Val Lys Ile Ser Cys Leu  
370 375 380

## (2) INFORMATION FOR SEQ ID NO:140:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

TGGACCACCC AGAAGTACCT TCATTATGAC 30

## (2) INFORMATION FOR SEQ ID NO:141:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GTCATAATGA AGGTACTTCT GGGTGGTCCA 30

## (2) INFORMATION FOR SEQ ID NO:142:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA



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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

GGACCACCCA GCTTCATTAT GACGAAGAAA C

31

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GTTTCTTCGT CATAATGAAG CTGGGTGGTC C

31

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

GTGGACCACC CAGGACGAAG AAACCTCTC

29

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

GAGAGGTTTC TTCGTCTCGG GTGGTCCAC

29



77

## (2) INFORMATION FOR SEQ ID NO:146:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

CGTTTCCTCC AAAGTTCCTT CATTATGAC

29

## (2) INFORMATION FOR SEQ ID NO:147:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

GTCATAATGA AGGAACTTTG GAGGAAACG

29

## (2) INFORMATION FOR SEQ ID NO:148:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

GGAAACGTTT CCTGCAAAGT ACCTTCATTA TG

32

## (2) INFORMATION FOR SEQ ID NO:149:



78

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

CATAATGAAG GTACTTTGCA GGAAACGTTT CC

32

## (2) INFORMATION FOR SEQ ID NO:150:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

CACGCAAAAG TCGGGAATAG ATGTCAC

27

## (2) INFORMATION FOR SEQ ID NO:151:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

GTGACATCTA TTCCCGACTT TTGCGTG

27

## (2) INFORMATION FOR SEQ ID NO:152:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid



79

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

CACCCTGTCG GAAGAGGCCT TCTTC

25

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

GAAGAAGGCC TCTTCCGACA GGGTG

25

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

TGACCTCTCG GAAAGCAGCG TGCA

24

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

TGCACGCTGC TTTCCGAGAG GTCA

24

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

CCTCGAAATC GAGCGAGCAG CTCC

24

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

CGATTTCGAG GTCTTTCTCG TTCTC

25

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

CCGTGAAAAT AAGCTCGTTA TAACTAGGAA TGG

33

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

CCATTCCTAG TTATAACGAG CTTATTTTCA CGG

33

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

CCTCTGAGCT CAAGCTTCCG AGGACCACAA TGAACAAG

38

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:



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CCTCTCTCGA GTCAGGTGAC ATCTATTCCA CACTTTTGCG TGGC

44

## (2) INFORMATION FOR SEQ ID NO:162:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

CCTCTGAGCT CAAGCTTCCG AGGACCACAA TGAACAAG

38

## (2) INFORMATION FOR SEQ ID NO:163:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

CCTCTCTCGA GTCAAGGAAC AGCAAACCTG AAGAAGGC

38

## (2) INFORMATION FOR SEQ ID NO:164:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

CCTCTGAGCT CAAGCTTCCG AGGACCACAA TGAACAAG

38



## (2) INFORMATION FOR SEQ ID NO:165:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

CCTCTCTCGA GTCACTCTGT GGTGAGGTTC GAGTGGCC

38

## (2) INFORMATION FOR SEQ ID NO:166:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

CCTCTGAGCT CAAGCTTCCG AGGACCACAA TGAACAAG

38

## (2) INFORMATION FOR SEQ ID NO:167:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

CCTCTCTCGA GTCAGGATGT TTTCAAGTGC TTGAGGGC

38

## (2) INFORMATION FOR SEQ ID NO:168:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids



84

(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Met Lys His His His His His His His Ala Ser Val Asn Ala Leu Glu

1            5            10            15